

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 05-01-03
Searcher: Beverly E 4994
Terminal time: 20
Elapsed time: _____
CPU time: _____
Total time: 25
Number of Searches: _____
Number of Databases: 1

Search Site

_____ STIC
_____ CM-1
_____ Pre-S

Type of Search

_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors

_____ IG Suite
_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
✓ _____ Other CGN

GenCore version 5.1.4 p5 4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 30, 2003, 09:41:39 ; Search time 3394 Seconds

(without alignments)
5890.874 Million cell updates/sec

Title: US-10-061-727-2

Perfect score: 3669

Sequence: 1 MTLWCVSVLYFYGIQSDA.....SALALHFTDLSNNNDPYIL 687

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DOCALIGN=200 -THR SCORE=DCT -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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36: em_hcg_mam.*
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41: em_hngo_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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10	1256	34.2	46509	9	AC108747
11	1042	28.4	58987	2	AC119283
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13	825	22.5	2061	9	AF212016
14	825	22.5	2080	9	HS2490436
15	825	22.5	2212	9	AF284436
16	825	22.5	2985	9	HS2472208
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22	772	21.0	3504	9	HS243874
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RESULT 1

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 KEYWORDS interleukin 1 receptor accessory protein.
 SOURCE Homo sapiens fetal brain cDNA to mRNA.
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (sites)
 AUTHORS Saito, T. and Seki, N.
 TITLE Molecular cloning of human interleukin 1 receptor accessory protein
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 4724)
 AUTHORS Saito, T.
 TITLE Direct Submission
 JOURNAL Submitted (12-AUG-1997) Toshiyuki Saito, National Institute of
 Radiological Sciences, Genome Research Group, Anagawa 4-9-1, Inage,
 Chiba 263, Japan (E-mail: t_saito@nirs.go.jp, Tel.043-206-3135,
 Fax:043-251-9818)
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 DB 267 TCAGACGCTGCGCATGACTGGGGGCTGAGACCAATGAGGCAATCCAAAGTCTTGAAGAT 326
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 QY 61 AlhHisSerIleGlyLeuThrLeuIleTrpTyrTyrThrArgGlnAspArgAspLeuGln 80
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 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 Unclassified.
 AUTHORS Cao, Z.
 TITLE Interleukin-1 receptor accessory proteins, nucleic acids and methods
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RESULT 3
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DEFINITION AF029213
ACCESSION AF029213
VERSION AF029213.1 GI:2599126
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1740).
AUTHORS Huang,J., Gao,X., Li,S. and Cao,Z.
TITLE Recruitment of IRAK to the interleukin 1 receptor complex requires
interleukin 1 receptor accessory protein
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (24), 12829-12832 (1997)
MEDLINE 98058729
PUBMED 9371760
2 (bases 1 to 1740)
AUTHORS Huang,J., Gao,X., Li,S. and Cao,Z.
TITLE Direct Submission
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 DEFINITION Sequence 3 from patent US 6280955.

ACCESSION AR166116
 VERSION AR166116.1 GI:16241290
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 3355)
 AUTHORS Cao, Z.
 TITLE Interleukin-1 receptor accessory proteins, nucleic acids and
 JOURNAL methods
 Patent: US 6280955-A 3 28-AUG-2001;
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SOURCE Mus musculus.
ORGANISM Mus musculus.
REFERENCE 1. (bases 1 to 3355)
AUTHORS Bakkayota; Metzosa; Chorata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Molecular cloning and characterization of a second subunit of the
JOURNAL J. Biol. Chem. 270 (23), 13757-13765 (1995)
MEDLINE 95293970
PUBMED 7775431
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Best Local Similarity: 71.57% Mismatches: 76
Query Match: 63.44% Indels: 28
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 1 (bases 1 to 1862)
 Liu, C., Chalmers, D., Maki, R. and De Souza, E. B.
 Rat homolog of mouse interleukin-1 receptor accessory protein:
 cloning, localization and modulation studies
 J. Neuroimmunol. 66 (1-2), 41-48 (1996)
 MEDLINE
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 Liu, C.
 Direct Submission
 Submitted (06-FEB-1996) Changlu Liu, Molecular Biology, Neurocrine
 Biosciences, Inc., 3050 Science Park RD, San Diego, CA 92121, USA
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          LKVELKRAKSLVLIKMKSEKSPQSRFMQLQVAMPVKKSPHSSSDKGLSYSS
          LKNV"

BASE COUNT      500 a      429 c      484 g      449 t
              C G G I N

-ignment Scores:
Pred. No.:      2,39e-172      length:      1862
Score:          2313.50      Matches:      430
Percent Similarity: 86.62%      Conservative: 62
Best Local Similarity: 75.70%      Mismatches: 55
Query Match:      63.06%      Indels:      21
DB:              10      Gaps:      5

US-10-061-727-2 (1-687) x RNU48592 (1-1862)

QY      1 MetThrLeuLeuTyrCysValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
DB      103 ATGGGACTTCCTGGGTTGATGAGTCTGTTCTCGAGGAGATCCGACGAGTCAAGCT 162
QY      21 SerGluArgCysAspAspTProGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
DB      163 TCCGAACGCTGTGATGACAGGAGACAGTACGATGACCAATTCAGAGTGTGAAAGAT 222
QY      41 GluProAlaArgIleLeuCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
DB      223 GAGCCAGCTCGATGACAGGCCCTCTTTGACACCTTCTTGAAAGTACACATACACAGACT 282
QY      61 AlaHisSerAlaGlyLeuThrLeuIleTyrTyrThrArgGlnAspArgAspLeuGln 80
DB      283 GCCCATTCCTCTGAGACTTACCTCGATCTGTACTGACACAGGACAGCGGAGCTCGAG 342
QY      81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLeuGlnLysAspValLeuTyr 100
DB      343 GAGCCCATTAATTTCCGCTTCAGAGAAATCGATCAGTAAAGAGAAAGATGTGCTCTGG 402
QY      101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
DB      403 TTCGGGCCCACTCTCTCAATGACACGGGCATTAACCTGCATGTGAGAAACACGACT 462
QY      121 TyrCysSerLeuValAlaPheProLeuGluValGlnLysAspSerCysPheAsnSer 140
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QY      141 PrometLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
DB      523 CCGATGAGCTCCACGATGACAGGCTGATATTTGAACAGGATATTCACAAATATCAAGTGT 582
QY      161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrPyrMetGly 180
DB      583 CCAATATGATGATGATATTTCTTCCAGCTGTCAAAACATCGCTCATGGTATTAAGGT 642
QY      181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
DB      643 TGTACTGAATATGATGATATTTCAATATGTTCAACCAAGGACATGAATTTGAGTTTTC 702

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QY      201 IleAlaLeuIleSerAsnAsnGlnValSerTyrThrCysValValThrTyrProGluAsnGly 220
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QY      221 ArgThrPheHisLeuThrArgThrLeuThrValLysValAlaGlySerProLysAsnAla 240
DB      763 CGGCTCTTTCACCTCACCGACGACTAGACTGTAAAGTGATGAGCTACCAAAAGATGCA 822
QY      241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
DB      823 GTAACCACTCATATCACTACCGCAATGACCGCGTGTCTATGAGAAAGAACAGAGAG 882
QY      261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
DB      883 GAGTGTGTTATTCCTGTAAAGTCAATTTCAATTAATGACCTTCACAAATGAGATC 942
QY      281 TrrTrrThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
DB      943 TGTGTGACCATTTGATGAGAAAGACCTGATGACGTCCTGTTGACATCATCTATTGAA 1002
QY      301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
DB      1003 AGCGTAAGTTATTTCTCAACGGAAGATGAGACAGAGACTCAGATTTTGACATCAAGAA 1062
QY      321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
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QY      381 TyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeu 400
DB      1243 TACTGCTGAGATAGTCTCTCTTATACCGGCTCATTTTGGAAACGATGAAACAATCTT 1302
QY      401 AspGlyLysGluTyrAspIleTyrValSerTyrAlaArgAsnAlaGluGlnGluGluPhe 420
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QY      421 ValLeuLeuThrLeuArgGlyValLeuGluLysGlnPheGlyTyrLysLeuCysIlePhe 440
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QY      461 SerArgArgMetIleValValLeuSerProAspTyrValThrGlnLysSerIleSerMet 480
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DB      1543 CTGAGAGCTCAAGGCTGGCTA-----GAAATATAGGCTCCCGGGGCAACATCAAC 1593
QY      497 LeuIleValAlaGluTyrArgProLeuGluHisProHisProGlyIleLeuGlnLeuLys 516
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QY      531 HisSerGlySerLysPheTrpLysAlaLeuArgLeuAlaLeuProLeuArgSerLeuSer 550
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Db 1753 ---AGTCCAGGTGCTCTAGCACT 1773
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 LOCUS
 DEFINITION Homo sapiens soluble interleukin-1 receptor accessory protein
 (IL1RAP) mRNA, complete cds.
 ACCESSION AF167343
 VERSION AF167343.1 GI:8050486
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE
 AUTHORS 1 (bases 1 to 1857)
 Jensen, L.E., Muzio, M., Mantovani, A. and Whitehead, A.S.
 IL-1 signaling cascade in liver cells and the involvement of a
 soluble form of the IL-1 receptor accessory protein
 J. Immunol. 164 (10), 5277-5286 (2000)
 JOURNAL 2021666
 MEDLINE 10799889
 PUBMED
 REFERENCE 2 (bases 1 to 1857)
 AUTHORS Jensen, L.E.
 TITLE Direct Submission
 JOURNAL Submitted (08-JUN-1999) Department of Pharmacology, University of
 Pennsylvania, 156 Johnson Pavilion, 3420 Hamilton Walk,
 Philadelphia, PA 19104, USA
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 1. 1071
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 polyA_signal /gene="IL1RAP"
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 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 51.57% Indels: 0
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 DB 1 ATGACACTCTGTGGTGTAGTGAAGCTCTACTTTATGGAATCCGCAAGTGAATGCC 60
 QY 21 SerGluArgCysAspAspTTPGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40

DB 61 TCAGAACGCTGGAGATGACTGGGAGCTAGACACCATGAGGCAATCAATGTTTGAAGAT 120
 QY 41 GluProAlaArgIleLysCysProLeuPheGlnIlePheLeuLysPheAsnTYrSerThr 60
 DB 121 GAGCCAGCTGGATCAAGTACCCTCTTGGACACTCTTTAAATTCACATACAGCA 180
 QY 61 AlaHisSerAlaGlyLeuThrLeuIleTPYrTYrTPThrArgGlnAspArgAspLeuGln 80
 DB 181 GCCCATTCAGCTGAGCTTACTGATCTGTGATTTGAGATGAGACGAGGACCTTGAG 240
 QY 81 GluProIleAsnPheArgLeuProGluLysAsnArgIleSerLysGlnLysAspValLeuTP 100
 DB 241 GAGCAATTAATCTTCGCTCCCGCAGAACCCGATTATGAGAGAAACATGTGCTGTG 300
 QY 101 PheArgProThrLeuLysAsnAspThrGlyAsnTYrThrCysMetLeuArgAsnThrThr 120
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 DB 721 GTGCCCTCTGATCATCTACCTTAATGATCATGTGGTATATGAGAAAGACAGAGAG 780
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 QY 281 TTPTPThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGln 300
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 DB 961 GTTACTCTGAGAGATCTCAAGGACGATATGTCTGTGACNGCTAGAAAGTCCAAAGCGAA 1020
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 RESULT 8
 BC021159 1916 bp mRNA linear ROD 07-AUG-2002
 LOCUS
 DEFINITION Mus musculus, similar to interleukin 1 receptor accessory protein,
 clone MGC:114036 IMAGE:4161899, mRNA, complete cds.
 ACCESSION BC021159

VERSION BC021159.1 GI:18088147
 KEYWORDS MGC.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 REFERENCE 1 (bases 1 to 1916)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (07-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550, USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Jeffrey B. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 Contact: amadasystemsbiology.org
 Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whitting

FEATURES
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CDS
 BASE COUNT 594 a 399 c 420 g 503 t
 ORIGIN

Alignment Scores:
 Pred. No.: 3.3e-121 Length: 1916
 Score: 1663.00 Matches: 298
 Percent Similarity: 93.71% Conservative: 30
 Best Local Similarity: 85.14% Mismatches: 22
 Query Match: 45.33% Indels: 0
 DB: 10 Gaps: 0

US-10-061-727-2 (1-687) x BC021159 (1-1916)

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 Db 133 ATGGAGCTTCGTGATATTGATGATGCTGCTCTTAAAGGATCTCTCAGAGTCATCT 192

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 Db 193 TCGAGCCCTGTGATGATCGGAGCTAGATACCATGCGACAATCAATCGTTTGAAT 252

Oy 41 GluProAlaArgIleIleYsCyProLeuPheGluHisPheLeuYsPheAsnTySerThr 60
 Db 253 GAGCGGCTCGAATCAAGTCCCTCTTTGAACACTTCTGAAAGTACATCAAGCACT 312

Oy 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyTrpThrArgGlnAspArgLeuGlu 80
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Oy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerIleGluYsAspValLeuTrp 100
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Oy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyTrpCysMetLeuArgAsnThr 120
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Oy 121 TyrCysSerIleValAlaPheProLeuGluValGlnIleYsAspSerCysPheAsnSer 140
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Oy 141 ProMetIleLeuProValHisIleYsLeuTyTrpIleGluTyrglyIleGlnArgIleThrCys 160
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Oy 281 TrpTrpThrIleAspGlyIleYsProAspAspIleThrIleAspValThrIleAsnGlu 300
 Db 973 TGGGAGCAATTAATGAGAAAGCCGATGAGCTGACATGCAATCATCTATTAAGAA 1032

Oy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleYs 320
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Oy 321 ValThrSerGluAspLeuTyArgSerTyValCysHisAlaArgSerAlaTyGlyGlu 340
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Oy 341 ValAlaIleAlaIleValIleValIleGlnIleYs 350
 Db 1153 GCTGAGCAGGCTGCCAAGTGAACAGAAA 1182

RESULT 9
 AK095107
 LOCUS AK095107 2226 bp mRNA linear PRI 15-JUL-2002
 DEFINITION Homo sapiens cDNA FLJ37788 f1s, clone BRH1P2028593, weakly similar to Homo sapiens IL-1 receptor accessory protein mRNA.
 ACCESSION AK095107
 VERSION AK095107.1 GI:21754300
 KEYWORDS oligo capping; f1s (full insert sequence).

Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, U., Li, Z., Lichtarge, O., Lien, C., Liu, J., Liu, W., Louiseged, H., Lozada, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhinney, E., McLeod, M.P., Meador, M., Meier, G., Metzger, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Moore, S., Morgan, M., Moorish, T., Morris, S., Moser, M., Neal, D., Nelson, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokemko, S., Oghu, M., Okwom, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L., Quiles, M., Ren, Y., Rivers, S., Rojebokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshitari, N., Sisson, I., Sodergren, B., Sonalke, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Sytek, A., Taber, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczek, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Naylor, S.L., Weinstein, G., and Gibbs, R.

TITLE
Direct Submission
JOURNAL
unpublished
REFERENCE
2 (bases 1 to 46509)
AUTHORS
Worley, K.C.
TITLE
Direct Submission
JOURNAL
Submitted (31-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE
3 (bases 1 to 46509)
AUTHORS
Worley, K.C.
TITLE
Direct Submission
JOURNAL
Submitted (03-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE
4 (bases 1 to 46509)
AUTHORS
Worley, K.C.
TITLE
Direct Submission
JOURNAL
Submitted (21-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT
On Jun 21, 2002 this sequence version replaced gi:21306532.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

FEATURES

SOURCE

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annot.atton.html>.

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DB: 9 Gaps: 0

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US-10-061-727-2 (1-687) x AC108747 (1-46509)

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DB 22841 GATACAGTGAAGCAGCTTTTATTCATTCACAGAGAGAGATGTTGTTCTG 22900
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DB 22901 ACCCGCTGATGTCAGAGAGAGAGATGTCAGATGTTAACTGGGCTGTCATG 22960
QY 489 CyGlnAsnSerIleAlaThrlsLeuIleValIleGluTyrArgProLeuGluHisPro 508
DB 22961 TGGCAACATCTCCATTCGACCAAGCTCATTTGTTGAGTACCGTCCCTTGACACCGC 23020
QY 509 HisProGlyIleLeuGluLeuLysGluSerValSerPheValSerTrpLysGlyGluLys 528
DB 23021 CACCGAGGATCTTCAGGCTCAAGAGTCTGCTCTTTCTTGAGCTGGAGGAGAGAAAG 23080
QY 529 SerLysHisSerGlySerLysPheTrpLysAlaLeuArgLeuAlaLeuProLeuArgSer 548
DB 23081 TCCAAACATTCGCTCTAAATCTGGAAAGCTTTGGGCTGCTCTCCCTGAGAGAT 23140
QY 549 LeuSerAlaSerSerGlyTrpAsnGluSerCysSerSerGlnSerAspIleSerIleuAsp 568
DB 23141 CTGAGTCCAGATTCGCTGAGAGAGAGTCTCTCTCCAGTCTGACATCAGCTGGAT 23200
QY 569 HisValGlnArgArgArgLeuArgLeuLysGluProProGluLeuGlnSerSerGluArg 588
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QY 609 ThrCysArgCysValThrTyrCysGluGlnGluAsnHisLeuArgLeuLysSerArg 628
DB 23321 ACTGCGCGCTGTTGTGACCTTCTGAGAGAGAGAGATCACTTGAAGAGAGAGAGAG 23380
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DB 23441 TCGAAGATTCATGATGATACAAATGAGCAGATTCGAGAGAGAGAGAGAGAGAGAG 23500
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DEFINITION
AC119283
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCES
AUTHORS

1 (bases 1 to 58987)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Mus musculus, clone RP24-345H5
Unpublished
2 (bases 1 to 58987)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barta, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Brown, A., Camarata, J., Campiano, A., Chang, J., Chazaro, B., Choepel, Y., Collangelo, M., Collins, S., Collamore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, D., Dodge, S., Fero, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hago, B., Horton, L., Hulme, M., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kelle, C., Laroque, K., Lamares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., MacDonald, P., Major, J., Margulis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meidrid, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Roselli, M., Roy, A., Santos, R., Schauer, S., Schpack, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strussner, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Triggilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE
JOURNAL
COMMENT

Submitted (25-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.P.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: L25964
Center clone name: 345_H_5

NOTE: This record contains 72 individual
sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will

DB: 2 Gaps: 2

US-10-061-727-2 (1-687) x AC119283 (1-58987)

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QY 469 SerProAspTyrValThrGluLysSerIleSerMetLeuGlnPheLysLeuGluValMet 488
 Db 7268 AGCCCTGACTATGTGACAGAAAGACATCAGATCTGAGATTATGCTGGGTGTATG 7209

QY 489 CysGlnAsnSerIleAlaThrLysLeuIleValValGlnTyrArgProLeuGlnHisPro 508
 Db 7208 TCCGAGAACTCCATTCCTCACTAAGCTCATTTGTGTGGAGAACCTGCGCTTGAGAACCC 7149

QY 509 HisPro-GlyIleLeuGlnLeuLysGlnSerValSerPheValSerTyrLysGlyLys 528
 Db 7148 CATCCAGGACATCATCAGCTGAGAGAGCTGTGTCTTTTGTAAAGCTGGAAGGAGAGAAA 7089

QY 528 sSerLysHisSerGlySerLysPheTyrLysAlaLeuArgLeuAlaLeuProLeuArgSe 548
 Db 7088 GTCCAAACATTCCTGCTCCAGATTCTGAAAGCTTGCGCTTGTGCTTCCCTGAGAAAG 7029

QY 548 rLeuSerAlaSerSerGlyTyrPasnGlnSerCysSerSerGlnSerAspIleSerLeuAs 568
 Db 7028 TCTGAGCCGCACTCGGCTCGGATGAGAGCTGTCTTCTCACTGACATCATGCTGGA 6969

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QY 608 aThrCysArgCysCysValThrTyrCysGlnGlyLysAsnHisLeuArgAsnLysSerAr 628
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 LOCUS ARI79668
 DEFINITION Sequence 3 from patent US 6326472.
 ACCESSION ARI79668
 VERSION ARI79668.1 GI:20221223
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 1 (bases 1 to 2061)
 AUTHORS Timans,J.C., Debets,J.Eduard,Maria,Antonius., Sana,T.R.,
 Bazan,J.Fernando, and Kastelein,R.A.
 TITLE Human receptor proteins: related reagents and methods
 JOURNAL Patent: US 6326472-A 3 04-DEC-2001;
 FEATURES Location/Qualifiers
 source 1..2061
 BASE COUNT 656 a 421 c 459 g 525 t
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US-10-061-727-2 (1-687) x ARI79668 (1-2061)

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QY 20 AlasGlnArgCysAspAspTyrProGlnLeuAspThrMetArgGlnIleGlnValPheGlu 39
 Db 79 TCTGTGATGAGCTGCAATTGATGATGAGT---CTAAGACATACATGCTTTGGCA 135

QY 40 AspGlnProAlaArgIleLysCysProLeuPheGlnHisPheLeuLysPheAsnTyrSer 59
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QY 60 ThrAlaHisSerAlaGlyLeuThrLeuIleTyrTyrTyrThrArgGlnAspArgLeu 79
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QY 80 GlnGlnProIleAsnPheArgLeuProGlnAsnArgIleSerLysGlnLysAspValLeu 99
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QY 120 ThrTyrCysSerLysValAlaPheProLeuGlnValAlaGlnLysAspSer---Cys 137
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QY 194 GlyMetAsnLeuSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysVal 213
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QY 273 LeuMetAspSerArgAsnGlnValTyrThrThrIleAspGlyLysLysProAspAspIle 292
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Db 1075 GGGGGCTGGAGAAATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1134
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Qy 414 ---AsnIleGlnuIleuIleuValIleuValIleuValIleuValIleuValIleuVal 432
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Db 1375 GATCTCAAGATATATATATATATATATATATATATATATATATATATATATATATAT 1434
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Qy 548 -----SerLeuSerAlaSerGly 554
Db 1717 GCAGAACAGGACTTTTGGAGAACTCAAGCTTATACCTTATATGCGATGACCAAGTACT 1776
Qy 555 TrpAsnIleuSerIleuSerIleuValIleuValIleuValIleuValIleuValIleuVal 574
Db 1777 TCAGCCACTGCTGATCTCAAGCTGATCTC----- 1809
Qy 575 SerArgLeuIleuProGlnuLeuGlnuSer----- 586
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Db 1957 CTACCCCTTAATTAACACCCGAAAGATACCGAGAAATTTTCAAC 1998

RESULT 13
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DEFINITION AF212016
ACCESSION AF212016 GI:7363363
VERSION AF212016.1 GI:7363363
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 2061)
Sana,T.R., Debets,R., Timans,J.C., Bazan,J.F. and Kastelein,R.A.
Computational identification, cloning, and characterization of
IL-1R9, a novel interleukin-1 receptor-like gene encoded over an
unusually large interval of human chromosome Xq22.2-q22.3
Genomics 69 (2), 252-262 (2000)
MEDLINE 20487552
PUBMED 11031108
REFERENCE 2 (bases 1 to 2061)
Sana,T.R., Debets,R., Timans,J.C., Bazan,J.F. and Kastelein,R.A.
Direct Submision
Submitted (03-DEC-1999) Molecular Biology, DNAX Research Institute,
901 California Ave., Palo Alto, CA 95051, USA
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Qy 214 ValThrTyrProGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValIleVal 233
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Qy 253 ValTyrGluIleGluProGlyGluGluLeuIleProCysThrValTyrPheSerPhe 272
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Qy 273 LeuMetAspSerArgAsnGluValTrpTrpThrIleAspGlyIleValIleValIleVal 292
Db 833 AGTGAAGAGCTCGGCGCAATGATCTACTG-----ATGAAGAGAGAAAG----- 877
Qy 293 ThrIleAspValThrIleAsnGluSerIleSerHisSerArgThrGluAspGluThrArg 312
Db 878 -----TTATATGAAGAACTGCGAGGTCATTAAGA-----GAAGGTGAAATTAAG 922
Qy 313 -----ThrdIleLeuSerIleIleValIleValIleValIleValIleValIleVal 321
Db 923 CTTTCAAGAGACATCTTGAGAAAGAAAGATGAATGGACATCTTGAATCTGACAT 962
Qy 322 ThrSerGluAspLeuIleValSerTyrValCysHisAlaArgSerAlaValGluVal 341
Db 963 GTGGAAGCTGACCTG-----GCGAATTATACCTGCGCATGTTGAAGAAACGAAATGAGCG 1036
Qy 342 AlaIleValAlaIleValIleGluValIleValIleValIleValIleValIleValIleVal 361
Db 1037 -----AAACATGCCAGTCTTTGCGCTTAAAGAAATTAATCTTAATTAATGAGCTTGA 1093
Qy 362 CysGlyPheGluValIleThrValLeuLeuValIleIleLeuIleValIleValIleValIleVal 381
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Qy 402 GlyIleGluTyrAspIleTyrValSerTyrAlaArg----- 413
Db 1214 AACCAAGAAATGATGATCTCTCTTACACAAAGTGAACCAAGATCTTGAAGCTGT 1273
Qy 414 -----AsnAlaGluGluGluGluPheValLeuLeuThrLeuArgIleValLeuGluAsnGlu 432
Db 1274 GACAACTCTGAAGAGAGAGCTTGTCTTGAAGTACTGCAAGATCTCTGAGAAAAACAC 1333
Qy 433 PheGlyTyrIleLeuCysIlePheAspArgAspSerLeuProGlyIleAsnThrValGlu 452
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Qy 453 AlaValPheAspPheIleGlnArgSerArgMetIleValIleLeuSerProAspTyr 472
Db 1394 GATCTCAAGATATGTTAACAAGACAGAACTTATATCTGCTAATCTCAGACTAT 1453
Qy 473 ValThrGluIleSerIleSerMetLeuGluPheValLeuGluValIleMetCysGlnAsnSer 492
Db 1454 ATTCTCAGCGGGGATGAGTAT-----TTGAACTGGAAGAAAGCACTCATATCATG 1507
Qy 493 IleAlaThr-----LysLeuIleValIleValIleValIleValIleValIleValIleValIleVal 509

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Db 1508 CTATGATGAGGAAATCAAGTATTTGATGAGTACAGATTAA----- 1558
Qy 510 ProGly-----IleLeuGluIleValIleValIleValIleValIleValIleValIleValIleVal 520
Db 1559 -----GGAAAGTGAATTCAGAGAGAGTGAATGATCTTAAGCGATCAATCTTCTGTC 1615
Qy 521 PheValSerTrpIleGlyIleValIleValIleValIleValIleValIleValIleValIleVal 540
Db 1616 CTGATCAAGTGAAGGAGTCCAAAGCAGCAAAATTAATTAATTTGAGTTGGAAGCACTTA 1675
Qy 541 ArgLeuAlaIleProLeuArg----- 547
Db 1676 GTATATGAATATGCCATCAAGAAAGAAAGATGCTACTCGGTGCAATGCTTGAAGTCC 1735
Qy 548 -----SerLeuSerAlaSerGly 554
Db 1736 GCAAGAAAGCACTTTTGGAGAACTCCAGCTTAATACCTTAATTTGCCATGACAGTACT 1795
Qy 555 TrpAsnGluSerCysSerSerGlnSerAspIleSerLeuAspHisValGlnArgArg 574
Db 1796 TCAGCCACTGTGTGTCATCTCAGGCTGATCTC----- 1828
Qy 575 SerArgLeuIleGluProGluLeuGluIleSer----- 586
Db 1829 -----CTGAATTCACCTTCAGATTCATGCAATGACGACATGT 1870
Qy 587 -----GluArgAlaIleGlySerProProAlaProGly**MetSer 600
Db 1871 TGCAGAGTTATTAACATGAATACAGCCAGCTTCGATCTTCTTGAAGCAAC 1930
Qy 601 LysHisArgGlyIleSerSerAlaThrCysArgCysCysValThrTyrCysGluGlu 620
Db 1931 CACCAT-----ACTATTTGTAACCTGCGCTGACCTGACCTGACGACGACG 1975
Qy 621 AsnHisLeuArgAsn-----LysSerArgAlaGluIleHis 632
Db 1976 CTACCCCTTAATTAACACCTGAAAGATACCGAGATTTGAC 2017

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RESULT 15
 AF284436 2212 bp mRNA linear PRI 11-OCT-2000
 LOCUS AF284436
 DEFINITION Homo sapiens TIGIR-1 mRNA, complete cds.
 ACCESSION AF284436
 VERSION AF284436.1 GI:10644689
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 2212)
 Born,T.L., Smith,D.E., Garika,K.E., Renshaw,B.R., Bertles,J.S. and
 Sims,J.E.
 Identification and characterization of two members of a novel class
 of the interleukin-1 receptor (IL-1R) family. Delineation of a new
 class of IL-1R-related proteins based on signaling
 JOURNAL J. Biol. Chem. 275 (39), 29946-29954 (2000)
 MEDLINE 20459050
 PUBMED 10862729
 REFERENCE 2 (bases 1 to 2212)
 AUTHORS Born,T.L., Smith,D.E., Garika,K.E., Renshaw,B.R., Bertles,J.S. and
 Sims,J.E.
 TITLE Direct Submission
 JOURNAL Submitted (05-JUL-2000) Molecular Biology, Immunex Corp, 51
 University St., Seattle, WA 98101-2936, USA
 FEATURES
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 1..2212
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Qy 548 -----SerLeuSerAlaSerSergly 554
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Qy 555 TTPshngIuserCysSerSergIuseraspIleSerLeuaspHisvalGlnargArg 574
Db 1928 TCAGCCTCTGTGTCTCATCTCAGGCTGATCTC-----1960
Qy 575 SerArgLeuLysGluProGluLeuGlnSerSer-----586
Db 1961 -----CCTGAATTCACACCCCTTCAGATTCAATGCAATCAGGCACTGT 2002
Qy 587 -----GluArgAlaAlaGlySerProAlaProGly**MetSer 600
Db 2003 TGCAGAGCTTATAACATAGATACCAAGCAGACCTTCCAGTACTTCTTAGGCAAC 2062
Qy 601 LysHisArgGlyLysSerSerAlaThrCysArgCysValThrTyrCysGluGlyGlu 620
Db 2063 CACCAT-----ACTTATTGTAACTGCTGTGACGCTACTCAACGACAG 2107
Qy 621 AsnHisLeuArgasn-----LysSerArgAlaGluLeHis 632
Db 2108 CTACCCCTTATAATACACCTGAAAGATACCAAGAAATTTTCAC 2149

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Search completed: April 30, 2003, 11:50:48
 Job time : 3479 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 30, 2003, 09:40:19 ; Search time 275 Seconds

(without alignments)
5625.901 Million cell updates/sec

Title: US-10-061-727-2

Perfect score: 3669
Sequence: 1 MTLIMCVSLYFYGILOSDA.....SALAHHTFDLSNNNDPYIL 687

Scoring table: BLOSUM62

Xgapop 10.0	Xgapext 0.5
Ygapop 10.0	Ygapext 0.5
Fgapop 6.0	Fgapext 7.0
Delop 6.0	Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=N.Geneseq.101002 -QPM=faetap -SUFFIX=ring -MINMATCH=0.1 -LOOPECT=0
-LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTENT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10061727 @cgn 1.1 200 @runat.23042003.083115.7882 -NCPUS=6 -ICPU=3
-NO_XUPXY -NO_MMAP -LARGEQUERY -NRG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-MARN_TIMEOUT=30 -THREADS=1 -HEADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2586	70.5	1740	23 AAS15608	Human interleukin-
2	2580	70.3	1713	17 AAT32026	Human interleukin-
3	2327.5	63.4	1713	17 AAT32028	Mouse interleukin-
4	2327.5	63.4	3355	23 AAS15609	Mouse interleukin-
5	1934	52.7	1077	17 AAT32027	Soluble interleukin-
6	1930	52.6	2733	21 AAO3048	Fusion polypeptide
7	1889	51.5	2155	19 AAV23659	Human interleukin-
8	825	22.5	2061	20 AAV23659	Human IL-1R08 codi
9	825	22.5	2061	24 AAD27170	Human interleukin-
10	817.5	22.3	1979	20 AAX84308	Human TIGRR codin
11	800	21.8	1737	20 AAX58247	Human IL-1R08 codi
12	800	21.8	1737	24 AAD27169	Human interleukin-
13	772	21.0	2091	21 AAA27919	Human Xrec2 CDNA c
14	772	21.0	3122	22 AAK51941	Human polynucleoti
15	767	20.9	2537	24 AAD27179	Human interleukin-
16	765	20.9	3120	22 ABA09029	Human oligophrenin
17	765	20.9	3120	22 AAK52925	Human polynucleoti
18	531	14.5	287	22 AAI24540	Probe #1473 for g
19	531	14.5	287	22 AAI49786	cDNA encoding a hu
20	528.5	14.4	1620	19 AAV48299	Interleukin-18 rec
21	528.5	14.4	1620	20 AAZ20661	Human receptor pro
22	528	14.4	1626	18 AAT88774	Human interleukin-
23	528	14.4	1626	20 AAX87651	Human interleukin-
24	528	14.4	1626	24 AAD31175	Human IL-18 recept
25	520	14.2	1563	20 AAZ20655	Interleukin-18 rec
26	495	13.5	2314	20 AAX58241	Human IL-1R09 codi
27	495	13.5	2314	24 AAD27173	Human interleukin-
28	495	13.5	2681	20 AAX87650	Human interleukin-
29	495	13.5	2681	20 AAZ00059	Human ACTU CDNA.
30	495	13.5	2681	24 AAD31174	Human IL-18 recept
31	495	13.5	2562	21 AAO09035	Human TANGO 191 cD
32	488.5	13.3	2356	10 AAN90114	cDNA of murine int
33	488.5	13.3	2356	15 AAO73762	Murine IL-1 recept
34	485.5	13.2	2356	10 AAN90028	cDNA of clone GEMB
35	484.5	13.2	1731	10 AAN90028	Murine interleukin
36	484.5	13.2	1782	15 AAO71907	cDNA encoding mus
37	484.5	13.2	1782	18 AAT45877	Mouse interleukin-
38	484.5	13.2	1782	22 AAC86848	cDNA encoding a mo
39	484.5	13.2	1782	22 AAF24246	Murine interleukin
40	482	13.1	4989	16 AAO85962	Mouse ST1L gene.
41	482	13.1	4989	18 AAD03365	DNA encoding trans
42	479.5	13.1	2830	18 AAT88775	Mouse receptor pro
43	479.5	13.1	2830	20 AAX87653	Mouse interleukin-
44	478	13.0	1557	19 AAV48294	cDNA encoding a mu
45	478	13.0	1557	20 AAZ20656	Interleukin-18 rec

ALIGNMENTS

RESULT 1	AAS15608	standard; CDNA, 1740 BP.
XX	XX	XX
AC	AAS15608;	
XX	XX	XX
DT	21-MAY-2002	(first entry)
XX	XX	XX
DE	Human interleukin-1 Receptor accessory protein (IL-1R acp) CDNA.	
XX	XX	XX
KW	IL-1R acp; human; interleukin-1 receptor accessory protein; NF-kappaB;	
KW	IL-1; IL-1R; ss; inflammatory response.	
XX	XX	XX
OS	Homo sapiens.	
XX	XX	XX
Key	Location/Qualifiers	
FT	10..1722	
CDS	/*tag= a	
FT		


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Qy 441 AspArgAspSerLeuProGlyGlyAsnThrValGluAlaValPheAspPheIleGlnArg 460
Db 1330 GACCGAGACAGCTGCTGCGGGGAAATGTCACAGATGAGACTTGGACTTCATTGAGAAA 1389
Qy 461 SerArgArgMetIleValValLeuSerProAspTyrValThrGluYssSerIleSerMet 480
Db 1390 ACCAGACGGCTCTGCTGTGTCTTCTTAAGCCCACTAGCTGCTCCAGGAAACCAAGCCCTC 1449
Qy 481 LeuGluPheLeuGluGlyValMetCysGlnAsnSerIleAlaThrLys----- 496
Db 1450 CTGGAGCTCAAGGCTGGCTA-----GAAATATGCTCTCTCGGGCAACATCAAC 1500
Qy 497 LeuIleValValGluTyrArgProLeuGluHisProHisProGlyIleLeuGlnLeuLys 516
Db 1501 GTCATTATGATACAGTACAAAGCTGGAAGAAACGAG-----GTGAAGAGCTGAG 1554
Qy 517 GluSer-----ValSerPheValSerTyrPheGlyGlyLysSerLysHisSerGly 533
Db 1555 AGGGCTAAGACGGTCTCAAGCTCATTAATGAAAGGGAAGAAATCCAGATCCACAG 1614
Qy 534 SerLysPheTyrPheValAlaLeuArgLeuAlaLeuProLeuArgSerLeuSerAlaSerSer 553
Db 1615 GCGAGGTTCTGGAAGACGCTGCGAGTGGCCATCCAGTGAAGAAAGTCCCAAGCGGCTCT 1674
Qy 554 GlyTyrPheGluSerCysSerSerGlnSerAspIle 565
Db 1675 AGCAGTATGATGACGAGGCGCTCTGTATTCATCTTTG 1710

RESULT 2
AAT32026
ID AAT32026 standard; cDNA, 1713 BP.
AC AAT32026;
XX
XX 14-OCT-1996 (first entry)
XX
XX Human interleukin-1 receptor accessory protein cDNA.
XX
XX Interleukin-1 receptor accessory protein; IL-1 antagonist;
XX inflammation; therapy; antiinflammatory; ss.
XX
XX Homo sapiens.
XX
XX Key location/Qualifiers
XX sig_peptide 1..60 a
XX mat_peptide 61..1710
XX /*tag= b

WO9623067-A1.
XX
XX 01-AUG-1996.
XX
XX 17-JAN-1996; 96WO-EP00181.
XX
XX 23-JAN-1995; 95US-0376268.
XX
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
XX Chizzone RA, Ju GW;
XX
XX MPI. 1996-162691/36.
XX
XX P-PSDB; AAM01911.
XX
XX Isolated interleukin-1 receptor accessory protein - used to develop
XX of interleukin-1
XX
XX Claim 2; Page 71-72; 115pp; English.
XX
XX A cDNA clone (AAT32026) codes for human interleukin-1 receptor
XX accessory protein (IL-1R ACP), a protein that inhibits the
XX ability of IL-1 to bind to or otherwise activate the IL-1R,

```

```

CC esp. the Type 1 IL-1R. It was obtd. from a human YT cell cDNA
CC library using a probe derived from a human partial genomic clone.
CC The cDNA can be used for the produ. of pure IL-1R ACP by expression
CC in a host cell. The IL-1R ACP is used to treat or prevent the
CC inflammatory or immunological activities of IL-1.
XX
XX Sequence 1713 BP; 502 A; 358 C; 405 G; 448 T; 0 other;
XX
Alignment Scores:
Pred. No.: 1,216-213 Length: 1713
Score: 2580.00 Matches: 487
Percent Similarity: 91.04% Conservative: 31
Best Local Similarity: 85.59% Mismatches: 45
Query Match: 70.32% Indels: 6
DB: 17 Gaps: 3

US-10-061-727-2 (1-687) x AAT32026 (1-1713)
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Qy 21 SerGluArgCysAspSerTyrPheLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db 61 TCGAAGCGCTGGGATGACCTGGGAGACTAGACACCATGAGGCAATCCAGTGTGAAAGAT 120
Qy 41 GluProAlaArgIleLeuValCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
Db 121 GAGCCAGCTGGATCAAGTCCACTCTTGAACCTCTTGAATTCATCACTACAGACAA 180
Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTyrTyrThrArgGlnAspArgAspLeuGlu 80
Db 181 GCCCATTCAGCTGGCTTACTGATCTGTATTTGACTAGGACAGGACCGGACCTTGAG 240
Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTyr 100
Db 241 GAGCCAAATTAATCTCCGCTCCCGAGAACCCCATTAATGATGAGAGAAATGTGCTGG 300
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
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Qy 121 TyrCysSerLysValAlaPheProLeuGluValAlaGlnLysAspSerCysPheAsnSer 140
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Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
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Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrPheMetGly 180
Db 481 CCAAAATGATGATGATATTTCTTCCAGTGTCAAAACCATATATCATCTGTGATATGGCC 540
Qy 181 CysTyrLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db 541 TGTATTAATAATACAGAAATTTATATATATATATATATATATATATATATATATATAT 600
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
Db 601 ATTGCTTAATTTCAATATATATATATATATATATATATATATATATATATATATATAT 660
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValAlaGlySerProLysAsnAla 240
Db 661 CGTACGTTTCATCTCCAGGACTGTGATGAAAGTATGAGGCTCTTCAAAAAATGCA 720
Qy 241 ValProValIleHisSerProAsnAspHisValValTyrGlyLysGluProGlyGlu 260
Db 721 GTCCCCCTGTATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 780
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 781 GAGTACTATTCCTCCGTGAGGCTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 840

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QY 281 TTTTTPThrlleaspglylylylyProaspasillethrlleaspyalThrilleasngu 300
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QY 301 SerIleSerHisSerArgThrGluaspGluThrArgThrGlnIleleuSerIlelylys 320
DB 901 AGRTAAGTATGATGATGAAACAGAAAGATGAAACAAAGAACTGATTTGACATCAAGAA 960
QY 321 ValThrSerGluaspLeuIleValSerSerTyrValIleHisAlaArgSerAlaIlysglylu 340
DB 961 GTTACCTCTAGGATCTCAAGCCAGCTATGTCATCTGATCTGAAAGTGCACAAAGCGAA 1020
QY 341 ValAlaIleValAlaIleValIlysglylylyValProAlaProArgTyrThrValGluLeu 360
DB 1021 GTTGCCAAAGCAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
QY 361 AlaCysGlyPheGlyAlaThrValIleleuValIleleuIleValIleValIleVal 380
DB 1081 GCTTGTGTTTGGAGGACAGTCTCTGATGTCATCTGATGTTGTTTACCATTT 1140
QY 381 TTTTTPleuGluMetValleuPheTyrArgAlaHisPheGlyThrAspGluThrIleleu 400
DB 1141 TACTGGCTAGATGATGCTCTATTTTACCGGGCTCATTTTGAACAGATGAACCATTTTA 1200
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DB 1201 GATGAAAAAGATGATATTTATTTATGATCTTATGCAAGAAATCGGAGAAAGAAATTT 1260
QY 421 ValleuLeuThrleuArgGlyValIleuGluAsnGluPheGlyTyrIlylyleuCysIlePhe 440
DB 1261 GTTTTACTGACCTTCCTGAGAGTTTGGAGAAATGAAATTTGGAATCAAGCTGTGCACTTT 1320
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QY 481 LeuGluPheIlyleuGlyValIleMetCysGlnAsnSerIleleuThr--LysleuIleVal 499
DB 1441 CTGAGAGCTCAAGGCTGCTGAGAAATATGCGCTCTCGGGGCAACATCAACGTCATTTTA 1500
QY 500 ValGluTyrArgProleuGluHisProHisProGlyIleleuGluIlySerIleSer 518
DB 1501 GTACAGTACAAAGCTGGAAGAAAGCAAG-----GTAAAGAGGCTGAAGAGGCTTAAG 1554
QY 519 -----ValSerPheValSerTyrIlyGlyIlySerIlyHisSerIlySerIlyPhe 536
DB 1555 ACGGTGCTCAAGCTCATTAATAGAAAGGAGAAATCCAAAGATATCCACAGGCGAGGTTTC 1614
QY 537 TrpIleAlaIleuArgleuAlaIleuProleuArgSerleuSerAlaSerSerGlyTyrAsn 556
DB 1615 TGGAGAGAGCTGACAGGCGGACATCCAGTAAAGAAAGTCCAGAGCGGTCTTACAGATGAT 1674
QY 557 GluSerCysSerSerGlnSerIle 565
DB 1675 GAGCAGGCGCTCTCGTATTCATCTTTG 1701

```

RESULT 3
AAT32028
ID AAT32028 standard; cDNA, 1713 BP.

AC AAT32028;
XX 14-OCT-1996 (first entry)
XX Mouse interleukin-1 receptor accessory protein cDNA.
XX Interleukin-1 receptor accessory protein; IL-1 antagonist;
KM Inflammation; therapy; antiinflammatory; ss.

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XX OS Mus sp.
XX FH Key Location/Qualifiers
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XX FT mat_peptide 61..1713
XX FT /*tag= a
XX FT /*tag= b
XX MO9623067-A1.
XX PD 01-AUG-1996.
XX PF 17-JAN-1996; 96MO-EP00181.
XX PR 23-JAN-1995; 95US-0376268.
XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX PI Chizomite RA, Ju GW;
XX DR WPI; 1996-362691/36.
XX DR P-PSDB; AAM01913.
XX PT Isolated interleukin-1 receptor accessory protein - used to develop
XX PT prods. to treat or prevent inflammatory or immunological activities
XX PT of interleukin-1
XX PS Example 7; Page 76-77; 115pp; English.
XX CC A cDNA clone (AAT32028) codes for mouse interleukin-1 receptor
XX CC accessory protein (IL-1R AcP), a protein that inhibits the
XX CC ability of IL-1 to bind to, or otherwise activate, the IL-1R.
XX CC esp. the Type 1 IL-1R. It was obtd. by screening cell-surface
XX CC proteins in COS-7 cells transfected by 373-L1 cDNA using
XX CC anti-murine IL-1R AcP monoclonal antibody 4C5, and isolation of
XX CC cDNA clones from positive lines. The murine cDNA was used to
XX CC obtain a partial genomic clone of the human homologue. A probe
XX CC derived from this genomic clone was then used to isolate the
XX CC full-length cDNA (AAT32026) for human IL-1R AcP (AAM01911).
XX SQ Sequence 1713 BP; 473 A; 366 C; 428 G; 426 T; 0 other;
XX Alignment Scores:
XX Pred. No.: 9,176-192 Length: 1713
XX Score: 2327.50 Matches: 429
XX Percent Similarity: 87.61% Conservative: 66
XX Best Local Similarity: 75.93% Mismatches: 55
XX Query Match: 63.44% Indels: 15
XX DB: 17 Gaps: 5

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US-10-061-727-2 (1-687) x AAT32028 (1-1713)

```

QY 1 MetThrleuLeuTrpCysValSerleuTyrPheTyrGlyIleleuGlnSerAspAla 20
DB 1 ATGGGACTTCTGTGATGATTTGATGAGTCTGTCTTTATGAGATCTCGAGATCAAGCT 60
QY 21 SerGluArgCysAspAspTyrGlyleuAspThrMetArgGlnIleGlnValPheGluAsp 40
DB 61 TCGGAGCGGTGATGATCACTGGGGAATGAAATCAATCCAAATCCAAAGCTTTGAAGAT 120
QY 41 GluProAlaArgIleIleCysProleuPheGluHisPheleuIlyPheleuTyrSerThr 60
DB 121 GAGCTGGCTCGAATCAAGTGGCCCTCTTTGAACATCTCTTAAGATGACATCAAGCACT 180
QY 61 AlaHisSerAlaGlyleuThrleuIleTyrTyrTyrThrArgGlnAspArgAspLeuGlu 80
DB 181 GCCCATTCCTCTGCGCTTACCTGATCTGTGATGACCAAGGCAAGACCGGACCTGAG 240
QY 81 GluProIleAsnPheArgleuProGluAsnArgIleSerIlyGlyIlyAspValleuThr 100
DB 241 GAGCCATTAATCTTCGCGCTCCAGAGATCCATCATGATGAAAGAAAGATGCTCTGG 300

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OY 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
    |||
DB 301 TTCGGGCCCCCTCTCTCATATGACACGGGCAATTAACCTGATGTTGAGAACACAACT 360
OY 121 TyrCysSerIleValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
    |||
DB 361 TACTGGAGCAAAAGTTCATTTCCCTGGAAGTGTTCAGAAAGACAGCTGTTCATTTCT 420
OY 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrIleGlnArgIleThrCys 160
    |||
DB 421 GGCATGAGATTCCTCCAGTGCACAAAGATGATATTAAGACATGGCATTTCAATGATCATGT 480
OY 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrIleMetGly 180
    |||
DB 481 CCAAAATGATAGACGATATCTTCTCCAGTGCACAAACATCGGTCACTTGATTAAGGAT 540
OY 181 CysTyrLysIleGlnAsnPheAsnAsnValIleProGluGluMetLysLeuSerPheLeu 200
    |||
DB 541 TGTACTGAAATAGTGAATCTTTCATTAATGTACTACCGAGGGCATGAACCTTGACCTTTTTC 600
OY 201 IleAlaLeuIleSerAsnGlnLysAsnTyrThrCysValValThrTyrProGluAsnGly 220
    |||
DB 601 ATCCCTTGTTGTTCAATATACGGAATTAACATATGTTGTTGTTGTTGTTGTTGTTGTTGTT 660
OY 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
    |||
DB 661 CGTCTCTTCACTGCACGAGTGTGATGCTGAAGGTGGTGGCTCACCAAAAGATGCA 720
OY 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
    |||
DB 721 TTGCCACCCAGATCTATTTCTCAAAATGACCGTGTGTCTATGAAAGAACCAAGAGAG 780
OY 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
    |||
DB 781 GAACTGTTATTTCTCGCAAGTCTATTTCAATTAATGATCTCCCAAAATGAGTCT 840
OY 281 TPTPTPTThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
    |||
DB 841 TGGTGACCATTCATGAAAGAACGCTGATGACGTCAAGTGCACATCTATTAATGAA 900
OY 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
    |||
DB 901 AGGTGAAATGTTATTTCTCAACGGAAGATGAAACAAAGCATCTGATTTTGAGCATCAAGAA 960
OY 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGluGlu 340
    |||
DB 961 GTCAACCCCGAGATCTCAAGCGCAACTATGTCATGCTGCAAAATCAAAAGGAGGAA 1020
OY 341 ValAlaValAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360
    |||
DB 1021 GCTGAGCAGGCTGCCAAGTGAAGAAAGAAAGTATACCAACCAAGTACACAGTGAAGATC 1080
OY 361 AlaCysGlyPheGluValAlaThrValLysLeuValIleLeuIleValValTyrHisVal 380
    |||
DB 1081 GCGTGTGTTTGGAGCCACGAGTCTTCTGTTAGTGTCTCATTTGTTGTTTACCATGTT 1140
OY 381 TyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrArgGluThrIleLeu 400
    |||
DB 1141 TACTGCTGAGATGAGTGTCTCTTTTACCAAGTCACTTGGAAACAATGAAATTTCTT 1200
OY 401 AspGlyLysGluTyrAspIleTyrValSerTyrAlaArgAsnIleGluGluGluGluPhe 420
    |||
DB 1201 GATGGAAGAGATGATATTTATTTATGTTTCTATGCAAGAAATGTGAAGAAAGCAATTT 1260
OY 421 ValLeuLeuThrLeuArgGlyValLysGluAsnGluPheGlyTyrTyrLysLeuCysIlePhe 440
    |||
DB 1261 GTGCTGCTACCGTGTGAGAGTTTGGAGAAATGAGATTGGAATACCAAGCTGTGCATCTTC 1320
OY 441 AspArgAspSerLeuProGlyGlyAsnThrValGluAlaValPheAspPheIleGlnArg 460
    |||
DB 1321 GACAGAGACAGCTGCTGCTGGAGAAATTTGTCACAGATGAGAACCTTGAGCTTCATTCAGAA 1380
OY 461 SerArgArgMetIleValValLeuSerProAspTyrValThrGluLysSerIleSerMet 480

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DB 1381 AGCAGACGACTCTGTGTTCTTAAGTCCCACTAGCTGCTCCAGGAAACAAAGCCCTC 1440
OY 481 LeuGluPheLysLeuGlyValMetCysGlnAsnSerIleAlaThrLys----- 496
    |||
DB 1441 CTGAGCTCAAGGCTGGCTTA-----GAAATATGAGCTCCCGGGCAACATCAAC 1491
OY 497 LeuIleValValGluTyrArgProLeuGluHisProHisProGlyIleLeuGlnLeuLys 516
    |||
DB 1492 GTCAATTTTATGTCAGTACAAAGCTGTGAAGACATGAG-----GTGAAGAGCTGAAG 1545
OY 517 GluSer-----ValSerPheValSerTyrPheGlyGluLysSerLysHisSerGly 533
    |||
DB 1546 CCGGCTAAGACCGTCTCAAGCTATTAAATGGAAGAGAGAAATCCAAATCTCTCAG 1605
OY 534 SerLysPheThrPheValAlaLeuArgLeuAlaLeuProLeuArgSerLeuSerIleSer 553
    |||
DB 1606 GGCAGAGTTTGAAGAGATGTGACGTTGACCTGACCTGCAAGAAAG-----AGTCCC 1656
OY 554 GlyTyrPasnGluSer 558
    |||
DB 1657 AGTGTGTTAGCAAT 1671

RESULT 4
AAS15609
ID AAS15609 standard; cDNA, 3355 BP.
XX
XX AAS15609;
AC
XX
XX 21-MAY-2002 (first entry)
DT
XX
XX Mouse interleukin-1 Receptor accessory protein (IL-1R ACP) cDNA.
DE
XX
XX IL-1R ACP; mouse; interleukin-1 receptor accessory protein; NF-kappaB;
KW
XX IL-1; IL-1RI; ss; inflammatory response.
OS
Mus sp.
PH
Key Location/Qualifiers
FT CDS 135..1847
    /*tag= a
    /product= "interleukin-1 receptor accessory protein"
PN
XX
XX US628095-B1.
PD
XX 28-AUG-2001.
XX
XX 16-DEC-1997; 97US-0991944.
XX
XX 16-DEC-1997; 97US-0991944.
XX
XX (TULDA-) TULARIK INC.
XX
XX Cao Z;
XX
XX MPI: 2001-595441/67.
XX
XX P-PSDB; AAU09967.
XX
XX
XX Isolated polypeptide designated interleukin receptor accessory
XX polypeptide is useful for regulating cell function
XX
XX Example: Fig 2; 21pp: English.
XX
XX
XX This sequence represents the mouse interleukin-1 receptor accessory
XX protein (IL-1R ACP) cDNA that was used to generate a cDNA fragment
XX used as a hybridisation probe to isolate, from a cDNA library,
XX the human IL-1R ACP cDNA of the invention. The interleukin receptor
XX accessory protein (IL-1R ACP) and its modulators (agonists/antagonists)
XX are useful for regulating cell function. Transient expression of either
XX IL-1RI or IL-1RAcP alone does not result in ligand-independent induction
XX of an NF-kappaB-dependent luciferase reporter gene in 293 cells, however
XX coexpression of both proteins resulted in a 20-fold increase in
XX activation of NF-kappaB activity to a level comparable to that induced

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CC by IL-1. These data suggest that aggregation of IL-1RI and IL-1R ACP as
CC a result of protein overexpression can elicit a signaling pathway
CC leading to NF-kappaB activation. Modulating signal transduction
CC involving NF-kappaB in a cell may be achieved by modulating the activity
CC of IL-1R using binding agents such as agonists and antagonists.
CC Hybridisation probes to the cDNA sequence can be used to identify wild-
CC type and mutant IL-1R ACP alleles in clinical and laboratory
CC samples. Mutant alleles are used to generate allele-specific
CC oligonucleotide (ASO) probes for high-throughput clinical diagnoses
CC of diseases or disorders with an inflammatory response. In
CC therapy, therapeutic IL-1R ACP nucleic acids are used to modulate
CC cellular expression or intracellular concentration or availability of
CC active IL-1R ACP. This invention also comprises a method of screening for
CC an agent that modulates the interaction of an interleukin receptor
CC accessory polypeptide (IL-1R ACP) to a binding target.

XX Sequence 3355 BP; 909 A; 742 C; 753 G; 951 T; 0 other;

Alignment Scores:

Pred. No.:	2,45e-191	Length:	3355
Score:	2327.50	Matches:	443
Percent Similarity:	83.36%	Conservative:	73
Local Similarity:	71.57%	Mismatches:	76
Match:	63.44%	Indels:	28
Gap:	23	Gaps:	8

US-10-061-727-2 (1-687) x AAS15609 (1-3355)

QY 1 MetThrIleuLeuTrpCysValValSerIleuTrpPheTyrglyIleuGlnSerAspAla 20
DB 135 ATGGAGATTCTGTGGTATTGATGATGCTGTGCTTCTATAGGATCTCGAGAGTCAATGCT 194
QY 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
DB 195 TCGAGCGCTGTGATGATGCTGGGACTAGTACATGCGCAATCAATGCTTTTAAAGAT 254
QY 41 GluProAlaArgGlyLeuCysProIleuPheGlnIlePheLeuLysPheAsnTrpSerThr 60
DB 255 GAGCGGCTCGAATCAAGTGGCCCTCTTGAACCTTCTGAAGTACCACTACAGCACT 314
QY 61 AlaHisSerAlaGlyLeuThrIleuLeuIleTrpTyrglyArgGlnAspArgAspLeuGln 80
DB 315 GCCATTCTCTGGCTTACCTGATCTGCTGACTGAGCAGGCAAGCAGGAGCTGGAG 374
QY 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerGlyLeuLysAspValLeuTrp 100
DB 375 GAGCCCATTAATCTTCCGCTCCAGAGATCCATCATAGAGAGAGAGATGCTGCTGG 434
QY 101 PheArgProThrIleuLeuAsnAspThrGlyAsnTrpTyrglyCysMetLeuArgAsnThrThr 120
DB 435 TTCGGGCCCTCTCTCAATGACAGGCAATTAACCTGCACTGTTGAGAACACAACT 494
QY 121 TyrCysSerIleValAlaPheProIleuGlnValIleGlnLysAspSerCysPheAsnSer 140
DB 495 TACTGACAGAAAGTTGCAATTCCTCCGGAAGTTGTTCAAGAGACAGCTGTTCAATTC 554
QY 141 ProMetLysLeuProValHisIleLysLeuTrpIleGlyTrpGlyIleGlnArgIleThrCys 160
DB 555 GCCAGGAAATTCACAGTGCACAGAGATGATATTAAGAGAGGATTCATCAATCAT 614
QY 161 ProAsnValAspGlyTrpPheProSerSerValLysProThrIleThrTrpIleMetGly 180
DB 615 CCAATGTAGAGCGATCTTCTCTTCAATGCAATGCAATCGGTCACTTGGTATTAAGGT 674
QY 181 CysTrpLysIleGlnAsnPheAsnValIleProGlyIleMetAsnLysSerPheLeu 200
DB 675 TGTACTGAATAGTGAATTCATATGATACACGAGGAGCATGAACTTGACCTTTTC 734
QY 201 IleAlaLeuIleSerAsnAsnGlyLeuTrpTyrglyValValIleThrTrpProGluAsnGly 220
DB 735 ATCCCTTGGTTTCAAAATTAAGAAATTAACATGTGTGTTTCAATATCTTAATAACGGA 794
QY 221 ArgThrPheHisIleuThrArgThrIleuThrValLysValIleGlySerProLysAsnAla 240

DB 795 CGTCTCTTACACCTCACAGAGACTGATGATTAAGGTGGTGGCTCACAAAGAGATGCA 854
QY 241 ValProProValIleHisSerProAsnAspHisValValTyrglyLysGluProGlyGly 260
DB 855 TTGCGACCCCAAGATCTTCTCCAAATGACCGTGTGTCTATGAGAAAGAACCGAGAG 914
QY 261 GluLeuLeuIleProCysThrValTyrglyPheSerPheLeuMetAspSerArgAsnGlyVal 280
DB 915 GAATGCTTATTCCTTCAAAAGTCAATTAATTCATTTATGACTCCCAATGAGCTC 974
QY 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGly 300
DB 975 TCGTGAACATTAATGAGAAAGACCTGATGACGTACACGACATCACTATTAATGAA 1034
QY 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
DB 1035 AGTGAAGTATTAATCTTCAACGGAAGATGAAACAGAGACTGATTTGAGCTTCAAGAA 1094
QY 321 ValThrSerGluAspLeuLysArgSerTrpValCysHisAlaArgSerAlaLysGlyGly 340
DB 1095 GTACACCCCGAGAGATCTCAGCGCACTATGTCTGTATCTGCAATACCAAGGGGAA 1154
QY 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTrpThrValGluLeu 360
DB 1155 GCTGAGCAGGCTGCCAAGGTGAACAGAAAGTCAACCAAGGTACACAGTGAATCTC 1214
QY 361 AlaCysGlyPheGlyAlaThrValLeuLeuValIleLeuIleValIleValTyrglyHisVal 380
DB 1215 GCGTGTGTTTGGAGGACACGCTCTTCTGTGATGCTGTTCATATGCTTATGCTTACAGT 1274
QY 381 TyrTrpLeuGluMetValLeuPheTyrglyArgAlaHisPheGlyThrAspGluThrIleLeu 400
DB 1275 TACGGCTGGAGATGCTCTTGTACAGACTACCTTGGAGAGATGAACAATCTT 1334
QY 401 AspGlyLysGlyLysTrpAspIleTyrglyValSerTyrglyAlaArgAsnAlaGluGluGluPhe 420
DB 1335 GATGGAAGAAGATGATGATTAATTAATGTTTCCATGCAAGAAATGGAAGAAGAAATTT 1394
QY 421 ValLeuLeuThrLeuArgGlyValLeuGluAsnGluPheGlyTyrglyLysCysValIlePhe 440
DB 1395 GTGCTGTGAGCGCTGCGTGGAGTTTGGAGATGATGATGATGATCAAGCTGTGATCTTC 1454
QY 441 AspArgAspSerLeuProGlyGlyAsnThrValGlnAlaValPheAspPheIleGlnArg 460
DB 1455 GACAGAGACACCTGCTGGGGGAATGTCACATATGACACCTGAGCTTCAATTCAGAA 1514
QY 461 SerArgArgMetIleValIleLeuSerProAspTrpValThrGlyLysSerIleSerMet 480
DB 1515 AGCAGAGACCTCGTGTGCTTGTCTTAAGTCCCACTACGTGCTCCAGGAGACAGACCTC 1574
QY 481 LeuGluPheLysLeuGlyValMetCysGlnAsnSerIleAlaThrLys----- 496
DB 1575 CTGAGAGCTCAAGGCTGGCTTA-----GAATATGCGCTCCGCGGCAATCATCAAC 1625
QY 497 LeuIleValValGlyTrpArgProLeuGlnHisProHisProGlyIleLeuGlnLysLys 516
DB 1626 GTCAATTAATGCAAGTAAAGCTGTGAAGCATGAAG-----GTGAAGAGCTGAAG 1679
QY 517 GluSer-----ValSerPheValSerTrpLysGlyGlyLysSerLysHisSerGly 533
DB 1680 CGGGCTAAGAGCGGTCTCAGCGTCATTAATAGAAAGAGAGAAATCAATATCTCCAG 1729
QY 534 SerLysPheTrpLysAlaLeuArgLeuAlaLeuProLeuArgSerLeuSerSerSer 553
DB 1740 GCGAGGTTCTGGAAGAGCTTCCAGGTGCTCAATGCGCAGTGAAGAG-----AGTCCC 1790
QY 554 GlyTrpAsnGluSerCysSerSerGlnSerAspIleSerLeuAspHisValGlnAlaArg 573
DB 1791 AGGTGTCT-----AGCAATGACAGAGAGG-TCTCTCTCATCATCTCCGAAATA 1840
QY 574 ArgSerArgLeuLysGlyProProGluLeuGlnSerSerGluArgAlaAlaGlySer--- 592

AC AAA09048;
 XX
 DT 01-AUG-2000 (first entry)
 XX
 DE Fusion polypeptide 569, IL-1 trap coding sequence.
 XX
 DE IL-1 trap; cytokine; antagonist; CNTF; receptor; fusion protein;
 KM cytostatic; immunomodulator; osteopathic; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 PN MO200018932-A2.
 XX
 PD 06-APR-2000.
 XX
 PF 22-SEP-1999; 99MO-US22045.
 XX
 PR 25-SEP-1998; 98US-0101858.
 PR 19-MAY-1999; 99US-0313942.
 XX
 (REGG-) REGENERON PHARM INC.
 -- Stahl N, Yancopoulos GD;
 XX
 DR MPI: 2000-293165/25.
 DR P-PSDB; AA92206.
 XX
 PT Isolated nucleic acid molecule for treating cytokine-related diseases
 PT or disorders encodes a fusion polypeptide capable of binding a cytokine
 PT to form a nonfunctional complex
 XX
 PS Example 6; Fig 26A-E; 152pp; English.
 XX
 CC This sequence encodes fusion polypeptide 569, which is capable of
 CC binding cytokine IL-1 to form a non-functional complex.
 CC The invention concerns production of antagonists to any cytokine that
 CC utilizes an alpha specificity determining component, which when combined
 CC with the cytokine, binds to a first beta signal transducing component to
 CC form a non-functional intermediate which then binds to a second beta
 CC signal transducing component causing beta-receptor dimerization, the
 CC soluble alpha specificity determining component of the receptor
 CC (SR-alpha) and the extracellular domain of the first beta signal
 CC transducing component of the cytokine receptor (beta-1) are combined to
 CC form heterodimers (SR-alpha:beta-1) that act as antagonist to the
 CC cytokine by binding the cytokine to form a non-functional complex. The
 CC receptor components are shared by cytokines such as the CNTF (ciliary
 CC neurotrophic factor) family of cytokines. The invention provides the
 CC basis for the development of IL-6 antagonists, as they show that if, in
 CC the presence of a ligand, a non-functional intermediate complex,
 CC consisting of the ligand, its alpha receptor and its beta-1 receptor
 CC component, can be formed, it will effectively block the action of the
 CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers
 CC of the extracellular domains of the alpha specificity determining
 CC components of their receptors and the extracellular domain of gp130.
 CC The resultant heterodimers, function as high-affinity traps, rendering
 CC the cytokine inaccessible to form a signal transducing complex with the
 CC native membrane-bound forms of their receptor. The nucleic acids and
 CC polypeptides are useful for treating cytokine-related diseases or
 CC disorders such as osteoporosis and primary and secondary effects of
 CC cancer including multiple myeloma or cachexia.
 XX
 SO Sequence 2733 BP; 823 A; 633 C; 624 G; 653 T; 0 other;
 XX
 Alignment Scores:
 Pred. No.: 5,06e-157 Length: 2733
 Score: 1930.00 Matches: 357
 Percent Similarity: 99.72% Conservative: 0
 Best Local Similarity: 99.72% Mismatches: 1
 Query Match: 52.60% Indels: 0
 DB: 21 Gaps: 0

QY 1 MetThrLeuLeuTrpCysValValSerLeuTrpPheTrpGlyIleLeuGlnSerAspAla 20
 |||
 DB 1 ATGGTGCTTCTGTGGTGTGTAGTGGTCTTACTTTATGCAATCTCCAAAGTATGCC 60
 QY 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
 DB 61 TCAGAACGCTGGAGTGACTGGGGACTAGACACCATGAGGCAAAATCCAGTGTTCAGAGAT 120
 QY 41 GluProAlaArgIleLeuGlyCysProLeuPheGlnIleSphenLeuLysPheAsnTrpSerThr 60
 DB 121 GAGCCAGCTCGCATCAAGATGCGCACTTTCAGAACCTTTCAGAAATTCATCAGCAGCA 180
 QY 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTrpTrpArgGlnAspArgAspLeuGlu 80
 DB 181 GCCCATTCAGCTGGCTTCTGATCTGTGATTCGATTCAGCAGGACCGGACCTTCAG 240
 QY 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerGlyGlyAspValLeuTrp 100
 DB 241 GAGCCAAATTAACTTCGGCTCCCGAGAACCGCATTAAGGAGAAAGATGTCGTGG 300
 QY 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTrpTrpCysMetLeuArgAsnThrThr 120
 DB 301 TTCGGCCCACTCTCTCATATGACCTGGCAACTATACCTGATGTTAAGGAACACTCA 360
 QY 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
 DB 361 TATGACGCAAGAGTTCATTTCTTGGAAGTTGTCAAAAGACAGCTGTTTCAATTC 420
 QY 141 PrometLysLeuProValHisLysLeuTrpIleGluTrpGlyIleGlnArgIleThrCys 160
 DB 421 CCATGAAGAACTCCAGTGCATTAATGATATGAGATATGGCACTTCAGAGATCACTTGT 480
 QY 161 ProAsnValAspGlyLysTrpPheProSerSerValLysProThrIleThrTrpTrpMetGly 180
 DB 481 CCAATGTAGAGAGATATTTCTTCAGTGTCAACAGCATATCACTTGATATGGGC 540
 QY 181 CysTrpLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
 DB 541 TGTATTAAATACAGAAATTTTATATGTAATACCCGAGGATATTAATCTGATGTTCTTC 600
 QY 201 IleAlaLeuIleSerAsnAsnGlyAsnTrpTrpCysValValThrTrpProGluAsnGly 220
 DB 601 ATTCGCTTAATTTCAATATGAGAAATTAACATGTGTGTTACATATCCAGAAATGCA 660
 QY 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
 DB 661 CGTAGCTTTCATCTCACAGAGACTGCTGCTGAAAGTAGTAGGCTCTCCAAAATAATGCA 720
 QY 241 ValProProValIleHisSerProAsnAspHisValValIleTrpGluLysGluProGluGlu 260
 DB 721 GGGCCCCCTGTATCATCTACCTATATATCATGTGGTCTATGAGAAAGAACCAAGAG 780
 QY 261 GluLeuLeuIleProCysThrValTrpPheSerPheLeuMetAspSerArgAsnGluVal 280
 DB 781 GAGCTACTCATTCCTGTAGCGGTATTTATTTGTTTCGATGAGATTCGCAATAGGTT 840
 QY 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValIleThrIleAsnGlu 300
 DB 841 TGGTGCACCATTAAGGAAAAAACCTGATGACATCATTTGAGTGCACCAATTACGAA 900
 QY 301 SerIleSerHisSerArgTrpThrGluAspGluThrArgTrpGlnIleLeuSerIleLysLys 320
 DB 901 AGTATTAAGTCATAGTAACAGAAATGAAATCAACAACTCAGATTTTATGATCAAGAAA 960
 QY 321 ValIleThrSerGluAspLeuLysArgSerTrpValCysHisAlaArgSerAlaLysGlyGlu 340
 DB 961 GTTACTCTGAGAGATCTCAAGGCGAGTATGCTGTCAATGCTAGAAAGGCCAAAGCGCAA 1020
 QY 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTrpThrVal 358
 DB 1021 GTTGCCAAAGAGCCCAAGGTGAGAAAGTGCAGGCTCCCAAGATACACAGCTG 1074

DB:	19	Gaps:	0
US-10-061-727-2 (1-687) x AAV23659 (1-2155)			
QY	1	MethThreuleuTrpCysValValSerleuTyPheTyGlyIleleuGlnSerAspAla	20
Db	303	ATGACACTTCTGGGCTGTGTAGTGTCTTACTTTTATGGAATCTCTGCAAGAGTATGCC	362
QY	21	SerGlnArgCysAspAspTrpGlyIleuAspThrMetCArgGlnIleGlnValPheGluAsp	40
Db	363	TCGAAAGCTGCATATACGCGGAACTACGACACCAAGAGGCAAAATCCAAAGTGTGAAAT	422
QY	41	GluProAlaArgIleLeuScyCysProLeuPheGlnHisPheLeuLysPheAsnTySerThr	60
Db	423	GAGCGACTCGCATCAAGTGCCACTCTTTGAAACCTCTTGAATTCACATCAGCACA	482
QY	61	AlaHisSerAlaGlyLeuThrLeuIleTrpTyTrpThrArgGlnAspArgAspLeuGlu	80
Db	483	GCCCACTCAGCTGGCTTCTCTGATCTGGTGTGAGTTCAGTACGAGACCGGAGCTTGAG	542
QY	81	GluProIleAsnThrArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp	100
Db	543	GAGCAATTAACTTCGCGCTCCCGGAAACCGCATTTAGTAAAGAAAGATGCTGGG	602
QY	101	PheArgProThrIleuLeuAsnAspThrGlyAsnTyTrpCysMetLeuArgAsnThrThr	120
Db	603	TTCCGCGCCACTCTCTCTCAATGACACTGGCAACTTACTCGATGTTTAAAGAACACTACA	662
QY	121	TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer	140
Db	663	TATTGACGAAAGTGTGCATTTCCCTTGAAAGTTGTTCAAAAAGACAGCTGTTCAATTCC	722
QY	141	ProMetLysLeuProValHisLysValLeuTyTyleGluTyArgIleGlnArgIleThrCys	160
Db	723	CCCATGTAACTCCACAGTCATAAACGTATATGAAATATGAGGATTCAGAGATCATCTTGT	782
QY	161	ProAsnValAspGlyTyTrpPheProSerSerValLysProThrIleLeuTrpTyMetGly	180
Db	783	CCAAATGTAATGATATATTTCTTCCAGATGTCMAAACGACATACCTTGGTATATGGGC	842
QY	181	CysTyLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLysSerPheLeu	200
Db	843	TGTTATAAATACAGATTTTATATATGTAATACCGAAGGATGAACTTGAGTTTCTTC	902
QY	201	IleAlaLeuIleSerAsnGlnLysAsnTyTrpCysValValIleThrTyProGluAsnGly	220
Db	903	ATTCCCTTAATTTCAATATATGAAATTCACATGTGTGTATCCATATCCAAATAATGCA	962
QY	221	ArgThrPheHisLeuThrArgThrLeuTrpValLysValValGlySerProLysAsnAla	240
Db	963	CGTAGCTTATCTCACACGAGACTCTGACTGTAAAGTATGAGCTCTCCAAAATATGCA	1022
QY	241	ValProProValIleHisSerProAsnAspHisValValTyGluLysGluProGlyGlu	260
Db	1023	GTCGCCCTGTGATTCATTCACCTATATGATCATGTGTGTTATGAGAAAGAACCAAGAGG	1082
QY	261	GluLeuLeuIleProCysThrValTyPheSerPheLeuMetCAspSerArgAsnGluVal	280
Db	1083	GAGCACTCAATCCCTGTGATGAGTCTATTTTATGTTTCTGATGAAATTCGCGCAATAGGT	1142
QY	281	TrpTrpThrIleAspArgLysLysLysProAspAspIleThrIleAspValThrIleAsnGlu	300
Db	1143	TGGTGACCACTGATGAAAAAAACCTGATGATCATCATTTGATGTCCACTTAACGAA	1202
QY	301	SerIleSerHisSerArgThrGlnAspGluThrArgThrGlnIleLeuSerIleLysLys	320
Db	1203	AGTATAGCTCATCTAGAACAGAAAGTAAACTAGAACTCAGATTTTGAAGATCAAGAAA	1262
QY	321	ValThrSerGluAspLeuLysArgSerTyValCysHisAlaArgSerAlaLysGlyGlu	340
Db	1263	GTTACCTCTGAGATCTCAAGCGCAGCTATGTCTGTCAATGCTAGAAAGTCCAAAGGCGAA	1322
QY	341	ValAlaLysAlaAlaLysValLysGlnLys	350

Db 1323 GTTCCAAAGCAGCCAGAGTGAAGAGAAA 1352
 RESULT 8
 AAX58245
 ID AAX58245 standard; cDNA; 2061 BP.
 XX
 AAX58245:
 XX
 22-JUL-1999 (first entry)
 XX
 Human IL-1RD8 coding sequence.
 XX
 IL-1RD9; IL-1RD8; IL-1RD10; interleukin-1; IL-1receptor DNA; therapy;
 KM IL-1 receptor-like protein; abnormal expression; immunological disorder;
 KM inflammatory disorder; morphological disorder; ss.
 XX
 Homo sapiens.
 XX
 MO9919480-A2.
 XX
 22-APR-1999.
 XX
 14-OCT-1998; 98MO-US20939.
 XX
 10-AUG-1998; 98US-0095987.
 PR 15-OCT-1997; 97US-0051829.
 PR 17-NOV-1997; 97US-0071635.
 PR 12-MAR-1998; 98US-0078008.
 PR 18-MAR-1998; 98US-0040714.
 PR 15-APR-1998; 98US-0081883.
 XX
 (SCHE) SCHERING CORP.
 PI Bazan JF, Debets JEMA, Kastelein RA, Sana TR, Timans JC;
 DR WPI; 1999-326545/27.
 DR P-PSDB; AAY14126.
 XX
 Interleukin-1 receptor-like polypeptides RD8, 9 and 10
 XX
 Claim 28; Page 93-96; 150pp; English.
 XX
 This sequence encodes a interleukin-1 (IL-1) receptor-like polypeptide,
 CC designated IL-1 receptor DNA designation 8 (IL-1RD8), of the
 CC invention. The IL-1RD8, IL-1RD9, and IL-1RD10 proteins, their fragments
 CC and mutetins, also related antibodies, other binding agents and
 CC (ant)agonists are used to treat conditions associated with abnormal
 CC expression of the polypeptide or abnormal expression of, or response to,
 CC their ligands, e.g., immunological, inflammatory or morphological
 CC disorders. They may also be used to screen for binding agents (potential
 CC drugs), diagnostic reagents (to detect the proteins or their ligands) and
 CC to isolate related sequences. Antibodies may also be used to raise
 CC anti-idiotypic antibodies, as carriers for toxins, radionuclides or other
 CC therapeutic agents, and for affinity purification.
 XX
 SO Sequence 2061 BP; 656 A; 421 C; 459 G; 525 T; 0 other;
 Alignment Scores:
 Pred. No.: 1, 9e-61 Length: 2061
 Score: 825.00 Matches: 228
 Percent Similarity: 46.78% Conservative: 106
 Best Local Similarity: 31.93% Mismatches: 244
 Query Match: 22.49% Indels: 136
 DB: 20 Gaps: 27
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 QY 1 MetThrIeuNeuTrpCys---ValIaSerIeuTyRPhetYrGlyIleuEngInSerAsp 19
 DB 19 TTGGCCCTTGTGTCTGTCTGTAGTCAGCAAAATCTGAAGATGGTCAAGAGAAAT 78
 QY 20 AlaserGIuargCysaspaepTrpGlyIleuasprThrMetarGlnIleGlnValPheGlu 39

Db 79 TCTGTGATGCGCTGCAATGACTGTGATGAT---CTCAAGACATACATAGCTTTGGCA 135
 QY 40 AspGIuProAlaargIleIyScYsProIeuPheGluHisPheIeuIySphaenTySer 59
 DB 136 GTGAACACAGTCCAGTGAATATGTCCTTTCTACAGTTATATTTGTCACCACTATAGC 195
 QY 60 ThrIaHisSerAlaGlyIleuThrIleuIleTrpTyTrpThrargGlnAspaArgSerIeu 79
 DB 196 ACGGCCAGAGCACTGGCTCAGGCTTATGTGTAC-----AAAACAAAGGTGATTTG 249
 QY 80 GluGIuProIleasnPheargIleuProGIuAsnArgIleSerIySgIySAspValIeu 99
 DB 250 GAAGACCCATCATCTTT-----TCAGAGTCAGATGAGTCAGAAAGAGATTCATA 303
 QY 100 TrpPheargProThrIeuIeuAsnAspThrGlyAsnTyTrhxCysMetIeuArgsnThr 119
 DB 304 TGGTTCACTACAGTCAGGACCAAGACAGATGATTCATCTGTGTTTAAGAACTCA 363
 QY 120 ThrTyCysSerIySValAlaPheProIeuGluValGlnIlySAspSer-----Cys 137
 DB 364 ACATATTGCAATGAGGTGTCATGATCTTCATGCTGACAGATGATGATCAGGCTGTGC 423
 QY 138 PheAsnSerProMetIySleuProValHisIySleuTyTrIleGluTyGly----- 154
 DB 424 TACACACAGACGATCCGC-----TATTACAAAATCTGAATCAT 465
 QY 155 ---IleGlnArgIleThrCysProAsnValAspGlyTyRPhetSerSerValIySPro 173
 DB 466 AAAAGAAAGAGATCTCTCCATGACAGATGATGATTTAAAGTCCAGTACAGAGCCT 525
 QY 174 ThrIleThrTrpTyMetGlyCysTyIySIIleGlnAsnAsnValIleProGlu 193
 DB 526 GATGTGTGTGTATGAGATGCAAGCCAAATGTGAGAGATATATATACAGAA 585
 QY 194 GlyMetAsnIeuSerPheIeuIleAlaIleuIleSerAsnAsnGlyAsnTyTrhxCysVal 213
 DB 586 GGAATGCTCTTCTGATCCAGAAATTTCAAGAAAGATGAGAAATTTACATATGAA 645
 QY 214 ValThrTyProGIuAsnGlyArgThrPheHisIleuThrArgThrIeuThrValIySVal 233
 DB 646 CTTAATAT-----GAAGAAACTT-----GTAAAGCAACATCTGAATTGAAGTT 693
 QY 234 ValGlySerProIySAsnAlaValPro---ProValIleHisSerProAsnAspHisVal 252
 DB 694 ACAGCTTTACTACAGACAGAGCTCCCAAGCATGTGTCCTCCATGAGATCAGCAAGT 753
 QY 253 ValIyTrGluIyGluProGIuIleuIleuIleProCysThrValIyRPhetSerPhe 272
 DB 754 GTTATGATGTCAGCTGGGTAGCCTGTGAACATCCCTGCAAGCATCTTGGATTC 813
 QY 273 LeuMetAspSerArgAsnGluValTrpTrhIleAspGlyIySleYsProAspIle 292
 DB 814 AGTGAAGATCTGGGCAATGATCTACTG---ATGAAGAGAAAG----- 858
 QY 293 ThrIleAspValThrIleAsnGlySerHisSerArgThrGluAspGluThrArg 312
 DB 859 -----TTTATTTGAAGAACTGCGAGCTCATTTAGA---GAAGGTGAATTAAG 903
 QY 313 -----ThnGlnIleuSerIleIySlySVal 321
 DB 904 CTTTCAAGAGCATCTTGAGAAAAGAGATTGAATTTGGCACTCATCTTTGACTCAGTT 963
 QY 322 ThrSerGIuAspIleuIySArgSerTyRValCysHisAlaArgSerAlaIySgIyGluVal 341
 DB 964 GTGAAGCTGACTG---CGCAATTATACCTGCCATGTTGAAGAAACCGAAATGACGCG--- 1017
 QY 342 AlaIySAlaIleValIySgIySValProAlaProArgTyTrhValGluIleuAla 361
 DB 1018 ---AAACATGCGCAGTGTGTCGTGTAAGAAAGATTATATTAATTAATTAAGCTTCA 1074
 QY 362 CysGlyPheGlyAlaThrValIeuIeuValIleuIleValIyTrhHisValTyR 381

KM leiomyomatosis; epilepsy; Bazex syndrome; detection; defective gene;
 KM cell-signal transduction; gene therapy; inhibitor; immune regulation;
 KM cell proliferation; inflammation; s6.
 XX
 OS Homo sapiens.
 XX
 PN WO9932629-A1.
 XX
 PD 01-JUL-1999.
 XX
 PF 23-DEC-1998; 98WO-US27625.
 XX
 PR 23-DEC-1997; 97US-0068634.
 XX
 PA (IMMUNEX CORP.
 XX (IMMUNEX CORP.
 PI Sims JE;
 WI 1999-418928/35.
 P-PSDB; AAY22164.
 PT New interleukin-1 receptor analog TIGIR nucleic acid and proteins
 used to, e.g. treat autoimmune disease
 PS
 PS Claim 1; Page 8-9; 79pp; English.
 CC This sequence encodes the human TIGIR protein of the invention. The
 CC TIGIR DNA sequences can be used: (a) as probes or primers for
 CC identifying nucleic acid that encodes proteins with TIGIR activity;
 CC (b) to identify human chromosome X, to map genes on this chromosome
 CC and to identify disease-related genes (particularly in the region
 CC Xq21.3-22 where genes are present associated with e.g. FG syndrome,
 CC premature ovarian failure-1, leiomyomatosis, epilepsy, Bazex syndrome,
 CC etc.) including detection of defective genes; (c) to study cell-signal
 CC transduction and the TIGIR system, and (d) in gene therapy. Sense and
 CC antisense oligonucleotides derived from the TIGIR coding sequence can be
 CC used to inhibit expression of the TIGIR gene. The TIGIR protein, or its
 CC soluble fragments, are used: (i) to study cellular processes (immune
 CC regulation, proliferation, death, migration, interaction with other cells
 CC and inflammation); (ii) to identify and purify proteins that associate
 CC with TIGIR ligands and receptors, and to measure their biological
 CC activity; (iii) in screening for, and rational design of, potential
 CC inhibitors of activity; (iv) therapeutically against diseases mediated by
 CC TIGIR polypeptide counter-structures; (v) as molecular weight markers in
 CC electrophoresis; (vi) for determining isoelectric points of unknown
 CC proteins; (vii) as controls for determining the extent of protein
 CC fragmentation (e.g. to aid characterisation of protein structures by mass
 CC spectrometry); (viii) for generation of antibodies (Ab); and (ix) to
 CC deliver diagnostic or therapeutic agents to cells that express TIGIR
 CC binding molecules. Ab are used for affinity purification of TIGIR;
 CC therapeutically to inhibit binding of TIGIR to its counter structures,
 CC and (if agonistic) to promote cell signalling.
 XX
 SQ Sequence 1979 BP; 636 A; 405 C; 439 G; 499 T; 0 other;
 Alignment Scores:
 Pred. No.: 8e-61 Length: 1979
 Score: 817.50 Matches: 223
 Percent Similarity: 46.67% Conservative: 99
 Best Local Similarity: 32.32% Mismatches: 233
 Query Match: 22.28% Indels: 135
 DB: 20 Gaps: 26
 US-10-061-727-2 (1-687) x AAX84308 (1-1979)
 QY CysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAspGluProAla 43
 DB 9 TGCATTGAGCTGCTGAGTGAT---CTCAAGACATACATGCGCTTGGCAGTGAACCATC 65
 QY 44 ArgIleLysCysProLeuPheGlnHisPheLeuLysPheAsnTrpSerThrAlaHisSer 63
 DB 66 CGAGTGAATGAGCCCTTTCTACAGTTATATTCGTACCAACTATAGACGCGCCAGAGC 125

QY 64 AlaGlyLeuThrIleuLeuTrpTrpThrArgGlnAspArgGluGluProIle 83
 DB 126 ACTGGCTCAGGCTTATGTGTAC-----AAAAACAAGGCTATTGGAGAGCCATC 179
 QY 84 AsnPheArgLeuProGluAsnArgIleSerLysGlnLysAspValIleTrpPheArgPro 103
 DB 180 ATCTTT-----TCAGAGGTGAGATGAGCAAGAGGAAATTCATATATGTTTCACTCA 233
 QY 104 ThrIleuLeuAsnAspTrpGlnLysAsnTrpThrCysMetLeuArgAsnThrThrTrpCysSer 123
 DB 234 GCTAGGCAACAAGACAGTGAATTCATGCTGTGTTTAAGAACTCAACATATTGATG 293
 QY 124 LysValAlaPheProLeuGlnValValGlnLysAspSer-----CysPheAsnSerPro 141
 DB 294 AAGGTGCAATGCTCTGACTGCTGAGAGAAATGATGACGAGCTGTGTACAAACAGCAGG 353
 QY 142 MetLysLeuProValHisLysLysLeuTrpIleGluTrpGly-----IleGlnArg 157
 DB 354 ATCCG-----TATTTAAGAAATCTGAAGTCACTAAGAAAGAGAG 395
 QY 158 IleThrCysProAsnValAspGlyTrpPheProSerSerValLysProThrIleThrTrp 177
 DB 396 ATCTCTGCTCCAGACATGAGATGACTTAAAAAGTCCATGACGAGCTGATGTTGTGG 455
 QY 178 TyrMetGlyCysTrpLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeu 197
 DB 456 TATAAGAGATGCAAGCCAAAATGTGGAGAGCATATATATATACAGAAAGAAATGCTCTT 515
 QY 198 SerPheLeuIleAlaLeuIleSerAsnAsnGlnValTrpThrCysValValThrTrpPro 217
 DB 516 CTGATCCAGAGAGTTCAG 572
 QY 218 GlnAsnGlyArgThrPheHisLeuThrArgThrLeuThrValValValGlySerPro 237
 DB 573 ---GAGGAAACTT-----GTAAGACAACTGATGAAATGATACAGCTTACTC 623
 QY 238 LysAsnAlaValPro---ProValIleHisSerProAsnAsnHisValValTrpLys 256
 DB 624 ACAGACAAAGCTCCAGAGCATTTGTCCTCCATGAGATGACAGCAAGTATTATAGATGTC 683
 QY 257 GluProGlyGluGluLeuLeuIleProCysThrValTrpPheSerPheLeuMetAspSer 276
 DB 684 CAGCTGGTGAAGCTCTGAGACATCCCTCGCAAGACATCTTCGATTCAGTGAAGAGCTT 743
 QY 277 ArgAsnGlnValTrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspVal 296
 DB 744 GGGCCAAATGATCTACTG3---ATGAAGAGAGAAAG----- 776
 QY 297 ThrIleAsnGlnSerIleSerHisSerArgThrGlnAspGluThrArg----- 312
 DB 777 TTTATTGAAGACTGCGAGTCACTTGA---GAGGTGAATTAAGCTTCTCAAGAG 833
 QY 313 -----ThrGlnIleLeuSerIleLysLysValThrSerGluAsp 325
 DB 834 CATCTGGAGAAAAGAAAGTGAATGACATCTTGACTGATGAGAGCTGAC 893
 QY 326 LeuLysArgSerTrpValCysHisAlaArgSerAlaLysGlyGluValAlaLysAlaLa 345
 DB 894 CTG---CGAATTATACCTGCAATGTAAGAAACGAAATGACG---AAACATGCC 944
 QY 346 LysValLysGlnLysValProAlaProArgTrpThrValGluLeuAlaCysGlyPheGly 365
 DB 945 AGCTTTTTCGCGTAAAAAGATTTAATCTTAATAATGAGCTTGCAGGGGGCCCTGGGA 1004
 QY 366 AlaThrValLeuLeuValValIleLeuLeuValValTrpHisValTrpTrpLeuGluMet 385
 DB 1005 GCATCTTCCTCTCTCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1064
 QY 386 ValLeuPheTrpArgAlaHisPheGlyThrAspGluTrpIleLeuAspGlyLysGlyTrp 405
 DB 1065 ATGCTCTTCTACAGAGCAGCATTGGAGCTGATGAATGAATGAATGAATGAATGAAT 1124
 QY 406 AspIleTrpValSerTrpAlaArg-----AsnAlaGlu 416

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Db 1125 GATGCCATCTCTCTTACACAAAGGAGCAAGATCTTACATCTGTGACATCTCTGAA 1184
Qy 417 GUGUGUGUUPheValLeuLeuThrLeuArgGlyValLeuGluAsnGluPheGlyTyrLys 436
Db 1185 GAAGAGCACTTGTCTTGAAGTACTGCGAGATGCTCTGAAAAAACAATATGATATTA 1244
Qy 437 LeuGlyLeuPheAspArgSerLeuProGlyGlyAsnThrValGluValPheAsp 456
Db 1245 CTCTTCATCCGAAAGAGACCTGATTCGAAAGTGAACATCACTGGAAGATCTCACAGA 1304
Qy 457 PheLeuArgSerArgMetLeuValLeuLeuSerProAspTyrValThrGlyLys 476
Db 1305 TATGTTGAACAAGAGAGAGATATATATGCTCTAATCCAGACATATATCTCAGACG 1364
Qy 477 SerLeuSerMetLeuGluPheLeuGlyValMetCysGluAsnSerLeuLeuThr 495
Db 1365 GGATGGAGTATTT-----TTCCAACTGGAAGAGAGAGAGAGAGAGAGAGAGAG 1418
Qy 496 -----LysLeuLeuValValGluTyrArgProLeuGluHisProHisProGly 511
Db 1419 GAATCAAAAGTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1466
Qy 512 -----IleLeuGluLeuLysGluSerVal-----SerPheValSerTyr 524
Db 1467 AATTCGCAAGAGAGTGAATCATCTAAAGCGTAGATCAAACTTCTGCTCGATCAAGTG 1526
Qy 525 LysGlyGlyLysSerLysHisSerGlySerLysPheTyrLysAlaLeuArgLeuAlaLeu 544
Db 1527 AAGGATCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1586
Qy 545 ProLeuArg----- 547
Db 1587 CCCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1646
Qy 548 -----SerLeuSerAlaSerSerGlyTyrPheAsnGluSer 558
Db 1647 CTTTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1706
Qy 559 CysSerSerGlnSerAspPheSerLeuAspHisValGlnArgArgSerArgLeuLys 578
Db 1707 GTGTCATCTCAGGCTGATCTC----- 1727
Qy 579 GluProProGluLeuGlnSerSer----- 586
Db 1728 -----CTGAAATTCACCCCTTCAAGTCAATGCAAAATCAGCAGCTGTTGAGAGTTAT 1781
Qy 587 -----GluArgAlaAlaGlySerProAlaProGly**MetSerLysHisArgGly 604
Db 1782 AAACATGAGATACGAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1835
Qy 605 LysSerSerAlaThrCysArgCysValThrTyrCysGluGlyGluAsnHisLeuArg 624
Db 1836 -----ACTTATTTGAACCTGCTGAGCTGAGCTACTCAAGGAGAGAGAGAGAGAG 1886
Qy 625 Asn-----LysSerArgAlaGluLeuHis 632
Db 1887 AACACCTGAAAGATACCAAGAGATTTTAC 1916

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OS Homo sapiens.
XX XX W09919480-A2.
XX XX 22-APR-1999.
XX XX
XX XX 14-OCT-1998; 98MO-US20939.
XX XX 10-AUG-1998; 98US-0095987.
XX XX 15-OCT-1997; 97US-0951829.
XX XX 17-NOV-1997; 97US-0971635.
XX XX 12-MAR-1998; 98US-0078008.
XX XX 18-MAR-1998; 98US-0040714.
XX XX 15-APR-1998; 98US-0081883.
XX XX (SCHE ) SCHERING CORP.
XX XX Bazan JF, Debets JEMA, Kastelein RA, Sana TR, Timans JC;
XX XX WPI; 1999-326545/27.
XX XX
XX XX Interleukin-1 receptor-like polypeptides RD8, 9 and 10
XX XX
XX XX Claim 28; Page 88-91; 150pp; English.
XX XX
XX XX This sequence encodes a interleukin-1 (IL-1) receptor-like polypeptide,
XX XX designated IL-1 receptor DNX designation 8 (IL-1RD8), of the
XX XX invention. The IL-1RD8, IL-1RD9, and IL-1RD10 proteins, their fragments
XX XX and mutants, also related antibodies, other binding agents and
XX XX (ant)agonists are used to treat conditions associated with abnormal
XX XX expression of the polypeptide or abnormal expression of, or response to,
XX XX their ligands, e.g. immunological, inflammatory or morphological
XX XX disorders. They may also be used to screen for binding agents (potential
XX XX drugs), diagnostic reagents (to detect the proteins or their ligands) and
XX XX to isolate related sequences. Antibodies may also be used to raise
XX XX anti-idiotypic antibodies, as carriers for toxins, radionuclides or other
XX XX therapeutic agents, and for affinity purification.
XX XX
XX XX Sequence 1737 BP; 566 A; 330 C; 397 G; 444 T; 0 other;
XX XX
XX XX Alignment Scores:
XX XX Pred. No.: 2,17e-59 Length: 1737
XX XX Score: 800.00 Matches: 207
XX XX Percent Similarity: 51.44% Conservative: 96
XX XX Best Local Similarity: 35.14% Mismatches: 208
XX XX Query Match: 21.80% Indels: 78
XX XX DB: 20 Gaps: 24
XX XX
XX XX US-10-061-727-2 (1-687) x AAX58247 (1-1737)
XX XX
Qy 1 MethrLeuLeuLeuTyrCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAsp--- 19
Db 7 CTCACACTATTA-----GTGTCAACAATGCTCACTGATCTTATACCTTCTGATTT 60
Qy 20 ---AlaSerGluArgCysAspAspTyrGlyLeuAspPheMetAlaGlnIleValPhe 38
Db 61 CTTCAGTGAATGCTGATTTGATGCTGATGAT-----CTCAAGACATACATGAGCTTTG 117
Qy 39 GluAspGluProAlaArgIleCysProLeuPheGluHisPheLeuLysPheAsnTyr 58
Db 118 GCAGTGAACACAGTCCGAGTGAATGCTCTTTTCTACAGTATATTCGACCACTAT 177
Qy 59 SerThrAlaHisSerAlaGlyLeuThrLeuLeuIleTyrTyrThrArgGlnAspArgAsp 78
Db 178 AGCAGCGCCAGAGACACTGGGCTCAGGCTTATGTGTAC-----AAAACAAAGTGAT 231
Qy 79 LeuGluGluProIleLeuAspPheArgLeuProGluAsnArgIleSerLysGluLysAspVal 98
Db 232 TTGAAGAGGCCATCATCTTT-----TCAGAGGTCTGAGATGAGCAAAAGAGAGATTTCA 285
Qy 99 LeuTyrPheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuAsn 116
Db 286 ATATGTTTCACTGAGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 345

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OY 119 ThrThrTyrCysSerLysValAlaPheProLeuGluValGlnLysAspSer----- 136
DB 346 TCAACATATTCATGATGAGAGTTCATGCTGACCTGTCGACGAGAAATGATCAGGCTCG 405
OY 137 CysPheAsnSerProMetLysLeuProValHisLysLeuTyrIleGluTyrGly----- 154
DB 406 TGCCTCAACAGCAGATCCGCG-----TATTTAGAAAATCTGGAAGTC 447
OY 155 -----IleGlnArgIleThrCysProAsnValAspGlyTyrPheProSerSerValLys 172
DB 448 ACTAAAGAAAGAGAGATCTCTGTCAGACATGATGATCAATTAAGATCCGATCAGAG 507
OY 173 ProThrIleThrTyrPheTyrMetGlyCysTyrLysIleGlnAspPheAsnValIlePro 192
DB 508 CTGATGTTGTGTGTATTAAGAAATTCACCAAAATGCGAAGAACTAATTAATACAG 567
OY 193 GluGlyMetAsnLeuSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCys 212
DB 568 AAGAGAAATGCTCTCTGATCCAGAAAGTTCAAGAAAGATGAGAAATTCACATGT 627
OY 213 ValValaThrTyrProGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLys 232
DB 628 GAACCTTAATAT-----GAGGAAAACTT-----GTAAAGACAACTGAATTTGAAA 675
OY 233 ValValaGlySerProLysAsnAlaValPro-----ProValIleHisSerProAsnAspHis 251
DB 676 GTTACAGCTTACTCAACAGCAAGCTCCCAAGCATTTGTTCCCATGAGATTCAGCCA 735
OY 252 ValValaTyrGluLysGluProGlyGluGluLeuIleProCysThrValTyrPheSer 271
DB 736 AGTGTTATAGATGTCAGAGCTGGTAAGCTCTGACATCCCTCGAAGACATCTTCGGA 795
OY 272 PheLeuMetAspSerLysArgAsnGluValTyrPThrIleAspGlyLysLysProAspAsp 291
DB 796 TTCAGTGAAGAGCTGGCCAAATGATCTACTG-----ATGAAAGAGAAAG----- 843
OY 292 IleThrIleAspValThrIleAsnGluSerIleSerHisSerArgThrGluAspGluThr 311
DB 844 -----TTTATTGAAAGACTGGCAGCTCAGCTTGA-----GAGGTGAAATA 885
OY 312 Arg-----ThrGlnIleLeuSerIleLysLys 330
DB 886 AGGCTTCTCAAGAGCATCTTGAGAAAGAAAGATTGAATTGACATCTTGTACTCA 945
OY 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
DB 946 GTTGTGAAGCTGACCTG-----GCGAATTATACCTGCGCATGTTGAAACCGAAATGACGG 1002
OY 341 ValAlaLysValAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360
DB 1003 -----AAACATGCCAGTGTGCTGCGTAAAGAAAGATTAACTATTAATAATGACCT 1056
OY 361 AlaCysGlyPheGlyAlaThrValLeuLeuValValIleLeuIleValValTyrHisVal 380
DB 1057 GCAAGGGGCGCTGGAGAGAACTTCTCTCTCTGTAAGCTGGTGGTCAATTACAAATGC 1116
OY 381 TyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeu 400
DB 1117 TACAACATTGAATGATGCTCTTCTACAGCAGCACTTGTAGAGCTGATGAATAATGAT 1176
OY 401 AspGlyLysGluTyrTrpIleTyrValSerTyrAlaArg----- 413
DB 1177 GACAAACAAAGAAATGATGCTCTCTCTTACCAAAAGTGCAGCAAGATACTTTAGAC 1236
OY 414 -----AsnAlaGluGluGluGluPheValLeuLeuThrLeuArgGlyValLeuGluAsn 431
DB 1237 TGTGACAAATCTGAGAGAGAGCACTTTGCTTGAAGTACGCAAGATGCTCGGAAAA 1296
OY 432 GluPheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThr--- 450
DB 1297 CACTATGATATTAATCTTCTATCCAGAAAGACCTGATTCCAAGTGGAAAGCATAC 1356

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OY 451 ValGluAlaValPheAspPheIleGlnArgSerArgArgMetIleValLeuLeuSerPro 470
DB 1357 ATGGAAGATCTCAAGATATGTTGAACAAGACAGAACTTATTAATGCTTAATCTCA 1416
OY 471 AspTyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyValMetCysGln 490
DB 1417 GACTATATTTCTGACGCGGAGTGAATTT-----TTGAACTGGAAGACAGACTCCAT 1470
OY 491 AsnSerIleAlaThr-----LysLeuIleValValGluTyrArgProLeuGluHis 507
DB 1471 AACATGCTAGTCAAGTGAAGAAATCAAAATGATTTGATGATGATGTAACAGATTTAAA 1527
OY 508 ProHisProGly-----IleLeuGlnLeuLysGluSerVal----- 519
DB 1528 -----GGGAAAGTGAATTCAGAGAGTGAATCACTAAAGCGTGAATCAAACTT 1578
OY 520 ---SerPheValSerThrLysGlyLysLysSerLysHisSerGlySerLysPheThrLys 538
DB 1579 CTGTCCCTGATCAAGTGAAGGATCCAAAGCAGCAAAATTAATCTTAAGTTTGGAAG 1638
OY 539 AlaLeuArgLeuAlaLeuProLeuArg 547
DB 1639 CACTTATGATGAATGCCCATCAAG 1665

RESULT 12
AAD27169
ID AAD27169 standard; DNA; 1737 BP.
XX
AC AAD27169;
XX
DT 09-APR-2002 (first entry)
XX
DE Human interleukin-1 receptor DNA designation 8 (IL-1RD8) DNA #1.
XX
KW Human; morphogenesis; immune system; interleukin-1 DNA designation 8;
IL-1RD8 protein; therapy; immunological disorder; ds.
XX
OS Homo sapiens.
XX
FH
FT Key Location/Qualifiers
FT CDS 1..1737
FT /tag= a.
FT /product= "Human IL-1RD8 protein"
FT /note= "CDS does not include start and stop codon"
FT /partial

US6326472-B1.
XX
PD 04-DEC-2001.
XX
PF 14-OCT-1998; 98US-0173151.
XX
PR 15-OCT-1997; 97US-062066P.
PR 17-NOV-1997; 97US-065776P.
PR 12-MAR-1998; 98US-078008P.
PR 18-MAR-1998; 98US-078416P.
PR 15-APR-1998; 98US-081883P.
PR 10-AUG-1998; 98US-095987P.
XX
PA (SCHER) SCHERING CORP.
XX
PI Timans JC, Debets JEMA, Sana TR, Bazan JF, Kastelein RA;
XX WPI, 2002-121110/16.
XX DR P-PDB; AAE16566.
XX
PT Antibody fragments which specifically bind to primate interleukin 1
PT receptor-like molecules are useful to treat conditions associated with
PT abnormal expression of the receptor or its ligand, particularly
PT immunological disorders
XX
PS Disclosure; Column 7-10; 102pp; English.
XX

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[illegible]

ID AAA27919 standard; cDNA; 2091 BP.
 XX
 AC AAA27919;
 XX
 DT 12-SEP-2000 (first entry)
 XX
 DE Human Xrec2 cDNA coding region.
 XX
 KW Xrec2; Interleukin-1 receptor; X chromosome; gene therapy;
 KW retinoblastoma; lissencephaly; subcortical lamina heteropia;
 KW mental retardation; chowchock syndrome; bazex syndrome;
 KW hypertrichosis; lymphoproliferative syndrome; immunodeficiency; ss.
 OS Homo sapiens.
 XX
 PN MO200036108-A2.
 XX
 22-JUN-2000.
 -- 14-DEC-1999; 99WO-US29549.
 XX
 PR 14-DEC-1998; 98US-0112163.
 PR 10-NOV-1999; 99US-0164675.
 XX
 PA (IMMUNEX CORP.
 XX
 PI Sims JE, Smith DE, Born TL;
 XX
 DR WPI, 2000-442387/38.
 DR P-PSDB; AAY95298.
 XX
 PT Isolated interleukin-1 (IL-1) zeta nucleic acids and splice variants
 PT TDZ1, TDZ2, TDZ3 and their encoding proteins, useful as probes for
 PT identifying genes associated with diseases such as glaucoma, and
 PT insulin-dependent diabetes mellitus.
 XX
 PS Claim 12(a); Page 8-9; 87p; English.
 XX
 CC The present sequence is that of the coding region of cDNA encoding
 CC human Xrec2, a member of the interleukin-1 (IL-1) receptor family
 CC that is encoded by a gene on the X chromosome. The sequence was
 CC obtained by high-throughput sequencing of chromosome region Xp11,
 CC PCR and 5' RACE reactions. The invention is directed to novel,
 CC purified and isolated IL-1 zeta, IL-1 zeta splice variants and
 CC Xrec2 polypeptides (see AAY95297-301), the nucleic acids (see
 CC AAA27918-22) encoding such polypeptides, processes for production of
 CC recombinant forms of such polypeptides, and their uses. Xrec2
 CC nucleic acids are used to: to express Xrec2 polypeptides; as probes
 CC to identify nucleic acids encoding proteins of the IL-1 receptor
 CC family; to identify human chromosome X; to map genes on chromosome
 CC X; to identify genes associated with diseases, syndromes, or other
 CC conditions associated with chromosome X, such as retinoblastoma,
 CC lissencephaly, subcortical lamina heteropia, mental retardation,
 CC chowchock syndrome, bazex syndrome, hypertrichosis,
 CC lymphoproliferative syndrome and immunodeficiency; as
 CC single-stranded sense or antisense oligonucleotides to inhibit
 CC expression of Xrec2 polypeptides; to help detect defective genes in
 CC an individual; and for gene therapy.
 CC
 SQ Sequence 2091 BP; 644 A; 432 C; 479 G; 536 T; 0 other;
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 Percent Similarity: 47.33% Conservative: 128
 Best Local Similarity: 29.35% Mismatches: 283
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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Comphen Ltd.

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Run on: April 30, 2003, 10:47:55 ; Search time 53 Seconds
(without alignments)
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Title: US-10-061-727-2

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Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	767	20.9	2537	4	US-09-173-151A-34
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9	528	14.4	1626	4	US-09-578-178-1
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ALIGNMENTS

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US-08-991-944-1
Sequence 1, Application US/08991944
Patent No. 6280955
GENERAL INFORMATION:
APPLICANT: Cao, Zhaoan
TITLE OF INVENTION: Interleukin-1 Receptor Accessory Proteins,
TITLE OF INVENTION: Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,944
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-014
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1740 base pairs
TYPE: nucleic acid


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CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,944
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-014
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEO ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 3355 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 135..1844
US-08-991-944-3

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Query Match: 63.44% Indels: 28
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DB 735 ATCCCTGTGTCAATATGCAAGAAATTAACAAATGTGTGTATCAATCTTAATAAGGGA 794
QY 221 ArgThrPheHisLeuThrArgThrLeuThrValIleValAlaGlySerProLysAsnAla 240
DB 795 CGCTCTTTCACCTCAACGAGCTGAGCTGTAAAGTGTGTGGCTCAACCAAGATGCA 854
QY 241 ValProProValIleHisSerProAsnAspHisValValIleGluLysGluProGlyGlu 260
DB 855 TTGCCACCCCAATCATATCTCCAAATGACCGTGTGTCTATGAGAAAGAACAGAGAG 914
QY 261 GluLeuLeuIleProCysThrValIlePheSerPheLeuMetAspSerArgAsnGluVal 280
DB 915 GAACTGTATATCCCTGCAAAAGCTATTTCACTTCAATTAAGTACCTCCCAATAGATGTC 974
QY 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
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 Oy 601 LysHisArgGlyLysSerSerAlaThrCysArgCysValThrTyrCysGluGlu 620
 Db 1912 CACCAT-----ACTATTTGTAACCTGCGCTGAGCCTGACTCAAGCAGCAG 1956
 Oy 621 AsnHisLeuArgAsn-----LysSerArgAlaGluIleHis 632
 Db 1957 CTACCCCTTAATTAACACCTTGAAAGATACCCAGAAATTCAC 1998

RESULT 4
 US-09-173-151A-1
 ; Sequence 1, Application US/09173151A
 ; Patent No. 6326472
 ; GENERAL INFORMATION:
 ; APPLICANT: Timans, Jacqueline C.
 ; APPLICANT: Debets, Johannes Eduard Maria
 ; APPLICANT: Antonius
 ; APPLICANT: Sana, Theodore R.
 ; APPLICANT: Bazan, J. Fernando
 ; APPLICANT: Kastelein, Robert A.
 ; TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: DNAX Research Institute
 ; STREET: 901 California Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/173,151A
 ; FILING DATE: 14-OCT-1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/065,776
 ; FILING DATE: 17-NOV-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/078,008
 ; FILING DATE: 12-MAR-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/081,883
 ; FILING DATE: 15-APR-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/095,987
 ; FILING DATE: 10-AUG-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/078,416
 ; FILING DATE: 18-MAR-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/062,066
 ; FILING DATE: 15-OCT-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ching, Edwin P.
 ; REGISTRATION NUMBER: 34,090
 ; REFERENCE/DOCKET NUMBER: DX0767X
 ; TELECOMMUNICATION INFORMATION:

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Qy 539 AlaLeuArgLeuAlaLeuProLeuArg 547
Db 1639 CACTAGTATATGAAATGCCATCAAG 1665

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RESULT 5

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US-09-173-151A-34
Sequence 34, Application US/09173151A
Patent No. 6326472
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
APPLICANT: Debets, Johannes Eduard Maria
APPLICANT: Antonius
APPLICANT: Sana, Theodore R.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,151A
FILING DATE: 14-OCT-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/062,066

```

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FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 2537 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2004
US-09-173-151A-34

Alignment Scores:
Pred. No.: 2,8e-69 Length: 2537
Score: 767.00 Matches: 210
Percent Similarity: 47.13% Conservative: 119
Best Local Similarity: 30.09% Mismatches: 274
Query Match: 20.90% Indels: 96
DB: 4 Gaps: 22

US-10-061-727-2 (1-687) x US-09-173-151A-34 (1-2537)
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Db 7 TGCACGACGTCGTCATCATCAT---ATCAAGAAATATCAAGTTTGGTGGAGAGCTGTT 63
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Db 64 CCAATCAAAATGTCACCTCTTATAGTGTATATACAGAACAAAATTAATCTCCCTCCCAAGT 123
Qy 64 AlaGlyLeuThrLeuIleTyrTyrThrArgGlnAspArgAspLeuGluProIle 83
Db 124 GCTGACCTAGTTTGTATGATGACAAAGTTCTGCTCTGAGACCTTGAAGACCAATA 183
Qy 84 AsnPheArgLeuProGluAsnArgIleSerLysGlyLysAspValLeuTyrPheArgPro 103
Db 184 GCCTTT-----GACGGAAGTGAATGAGCAGAAAGAAAGACTCCATTGTCGGGCA 237
Qy 104 ThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThrTyrCysSer 123
Db 238 ACATTGCTACAGAGAGAGTGTCTTACGCGCTGTGCATCAGAGACTCCACTTAAGTATAG 297
Qy 124 LysValAlaPheProLeuGluValAlaGlnLysAspSer-----CysPheAsnSerPro 141
Db 298 AAAGATCATCATCTCAGCAGTGGGTGAAATATGACACAGCTGCTATTAATTCAG 357
Qy 142 MetLysLeuProValHisLysLeuTyrIleGlyTyrGly-----IleGlnArg 157
Db 358 ATGAG-----TATTTGAAAAGCTGAACCTTAGCAAAAAGCAGAA 399
Qy 158 IleThrCysProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyr 177
Db 400 ATTTCATGCGGACATAGAGATTTTCTACAGCAACAGAGAACTGAATTCCTTTGG 459
Qy 178 TyrMetGlyCysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeu 197
Db 460 TACAAGAGATGAGAGCAAAAACATGAGGCGCAATGTTGTTCAAAAGAGATCTCTG 519
Qy 198 SerPheLeuIleAlaLeuIleSerAsnGlnLysAsnTyrThrCysValValThrTyrPro 217
Db 520 CTTATAGAGAGAGTCAAGAGATGACATTGGAATTTATACCTGGAATTAATAT 576
Qy 218 GluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValValValGlySerPro 237
Db 577 ---GGAGGCTTTGTTGTGAGAGAACTACTGAATTAAGCTTACA-----GCCCT 624

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QY 238 LysAsnAlaValProValIleHisSerProAsnAspHis-----ValValTyrGlu 255
Db 625 CTGACGTATAGCCACCAAGCTTTGATCTATGGAAGTAACATGACATTCAGAG 684
QY 256 LysGluProGlyGluGluLeuIleProCysThrValTyrPheSerPheLeuMetAsp 275
Db 685 ACCAGCGGTGAGCTCGCTAATCTAACCAGAGCTTCTTGCGTACAGCGAGAT 744
QY 276 SerArgAsnGluValTyrTrpThrIleAspGlyLysLysProAspAspIle----- 292
Db 745 GTCAAGCTCTTAATTTAATCTGATGAAAGAGAAAATTTATTAAGATCTGATGAAAT 804
QY 293 -----ThrIleAspValThrIleAsnGluSerIleSerHisSerArgThrGluAsp 309
Db 805 CGAGTTGGGAAAGTAAATTAAGAAAT-----CTTAAGAGCATCTTGGGAAACAG 855
QY 310 GluThrArgThrGlnIleLeuSerIleLysLysValThrSerGluAspLeuLysArgSer 329
Db 856 GAAGTTTCCATCTCATTAAT---GTGAGCTCTGTGGAAGAAGGTACTTG---GGAAT 909
QY 330 TyrValCysHisAlaArgSerAlaLysGlyGluValAlaLysAlaAlaLysValLysGln 349
Db 910 TACTCTGTATGTTGAAATAATGAAATGAGAGCT-----CGACAGCGCAGCGTCTCCTT 963
QY 350 LysValProAlaProArgTyrThrValGluLeuAlaCysGlyPheGlyAlaThrValLeu 369
Db 964 CATTAACAGAGCTAATGATACAGGTGAGACTCTGAGGCTTGTGGCTATATCTCTTG 1023
QY 370 LeuValValIleLeuIleValIleValTyrTrpLeuGluMetValLeuPheTyr 389
Db 1024 CTGCTTGATGTTGGTACCATCTACAGGTTCACAGATTAAGATTAATATCTCTTCTAC 1083
QY 390 ArgAlaHisPheGlyThrAspGluThrIleLeuAspGlyLysGlyTyrAspIleTyrVal 409
Db 1084 AGAATCATTTTGGAGCTGAGAGCTCGATGAGACATTAAGATTAATGATGATCTACTTA 1143
QY 410 SerTyrAlaArg-----AsnAlaGluGluGluGluPhe 420
Db 1144 TCATTAACCAAGAGTGATCTGACCATGGAATCAAGAGCTGGGAAAGAAAGCTTTT 1203
QY 421 ValLeuLeuThrLeuArgGlyValLeuGluAsnGluPheGlyTyrLysLysCysIlePhe 440
Db 1204 GCCCTTGAAATCTTACCTGATATGCTTGAAGATTAATGATTAATGATTTATATCA 1263
QY 441 AspArgAspSerLeuProGlyGlyAsnThrValGluAlaValPheAspPheIleGlnArg 460
Db 1264 GATAGAGATTAAATCCCAACTGAAATCATGTAAGATGTGGCAAGATGTGATGATCAA 1323
QY 461 SerArgArgMetIleValIleLeuSerProAspTyrValThrGluLysSerIleSerMet 480
Db 1324 AGCAAGCGGCTGATATTATGATGACCCCAATTAATGATTAAGAGGCTGAGCAATC 1383
QY 481 LeuGluPheLysLeuGlyValMetCysGluAsnSerIleAlaIle-----LysLeu 497
Db 1384 -----TTTGAGCTGGAACACAGACTTGGAATATGCTTGAGCTGGAAGAAATTAAGTG 1437
QY 498 IleValValGluTyrArgProLeuGluHisProHisProGlyIleLeuGluLeuLysGlu 517
Db 1438 ATTCATTAATTAATGATGAGTGAAGTGA-----GGAATTAATTAATCAACAGAGAG 1485
QY 518 -----SerValSerPheValSerThrLysGlyGluLys 528
Db 1486 GTGAGAGCCCTGGAACACACATCAAGCTCTGAGGCTCATTAATTAAGTACAGCAAA 1545
QY 529 SerLysHisSerGlySerLysPheTyrPheLysAlaLeuArgLeuAlaLeuProLeuArg--- 547
Db 1546 TGCAACAGATTGAATCTCAAGTTCTGGAACGTTTACAGTATGAATATCCCTTTTAAGAGG 1605
QY 548 -----Ser 548
Db 1606 ATAGAACCATTAACATGAGCAGGCTTATGATGTCATGAGCAAGGCGCTTTTGGGAGG 1665

QY 549 LeuSerAlaSerSerGlyTyrAsnGluSerCysSerSerGlnSerAspIleSerLeuAsp 568
Db 1666 CTCCACATGCTGTCCGCCCATTTTCCATGCGCGCGCCACCTCCACAGCTACGACCTGCC 1725
QY 569 HisValGlnArgArg-----ArgSerArgLeuLysGluProPro 581
Db 1726 CATCCAGATCTCCGTTCTACTCTTTCACAAACAGCTACCATTCACAAATGCGTCAAGAAC 1785
QY 582 GluLeuGlnSerSerGlnArgAlaAlaGlySerProProAlaProGly**MetSerLys 601
Db 1786 TACTACCGAAGCTATGATGACAGCTA-----CTTCTTACCGGCACTGCTCTTACC 1839
QY 602 HisArgGlyLysSerSerAlaThrCysArgCysCysValThrTyrCysGluGluGlu-As 621
Db 1840 TCATATGGAATGAGATATACCTATTAACATCCCTATGACATCTCATCAACGGGCAAGCGG 1899
QY 621 HisLeuArgAsnLysSerArgAlaGluIleHisAsnGluProGlnTrpGluThrHisLe 641
Db 1900 CCACAGACAAATGAGCAGGAGCAGAAATCCAGATGAGGCCCAACAAACAGTGCATC 1959
QY 641 UCysLysProValProGluGlu-----SerGluThrGlnTrpIleGln 655
Db 1960 CTGCCGCTG-TTGCACAGGAGACAGATATATCCAGTGTGATGATGAGAG 2010

RESULT 6
US-08-996-338-7
Sequence 7, Application US/08996338
Patent No. 6087116
GENERAL INFORMATION:
APPLICANT: TORIGOE, Kakuji
APPLICANT: OKURA, Takao
APPLICANT: KURIMOTO, Masashi
TITLE OR INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,338
FILING DATE: 22-DEC-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 74,697/1997
FILING DATE: 12-MAR-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 215,488/1997
FILING DATE: 28-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 291,837/1997
FILING DATE: 09-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOE=3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:

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? ORGANISM: lymphoblastoid cell derived from a patient
? ORGANISM: with Hodgkin's disease
? INDIVIDUAL ISOLATE: L428 (FERM BP-5777)
?
? FEATURE:
? NAME/KEY: sig peptide
? LOCATION: 1..57
? IDENTIFICATION METHOD: E
?
? FEATURE:
? NAME/KEY: mat peptide
? LOCATION: 58..1620
? IDENTIFICATION METHOD: E
?
? US-08-996-338-7

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Alignment Scores:	
Pred. No.:	7.47e-45
Score:	528.50
Percent Similarity:	46.11%
Percent Similarity:	30.05%
Percent Local Similarity:	14.40%
Y Match:	3
length:	160
Matches:	93
Conservative:	21
Mismatches:	21
Indels:	97
Gaps:	27

US-10-061-727-2 (1-687) x US-08-996-338-7 (1-1620)

Qy	4	LeuTrpCysValValSerLeuTyrPheTyrGlyIleuGlnSerAspAlaSerGluArg	23
Db	28	CTTTGGGCTTAAATCTGTA-----AGACTGCAGAAATCT	63
Qy	24	CysAspAspTrpGlyLeuAspThrMetArg---GlnIleGlnValPheGluAspGluPro	42
Db	64	TGT-----ACTTCAAGTCCCACTACTGTGGTGAAGGGGAACCT	105
Qy	43	AlaArgIleLys---CysProLeuPheGlnHisPheLeuLysPheAsnTyrSerThrAla	61
Db	106	TTCTATCTGAACATTCG-----TCGTGTCACTTGCA	138
Qy	62	HisSerAlaGlyLeuThrIleu---IleTrpTyrTrpThrArgIlnAspArgAspLeuGlu	80
Db	139	CATGAGATTGAACAACACCAACAAAGCTGGTGAACAAAGACGTGATCAGAGAACATGTG	198
Qy	81	GluProIleAsnPheAsnGlyLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp	100
Db	199	GAG---CTGAACCCAGAG---AGTTCTCGAGAAATTCCTTGACATGATGTGGTTGGAG	252
Qy	101	PheArgProThrLeuLeuAsnAspThrGlyAsnTyrTrpCysMetLeuArgAsnThr	120
Db	253	TTTGGCCAGTTGAGTTGAATGACACGAGATCTTACTTTTCCAAATGAAAATTTATACT	312
Qy	121	TyrCysSerLysValAlaPheProLeuGlnValValGln-----LysAspSerCysPhe	138
Db	313	CAG-----AAATGAATTAATATCTCATCAGAAATAAATAACACAGCTGTTTC	360
Qy	139	Asn-----SerProMetLysLeuProValHisLysLeuTyrIleGluTyrGly	154
Db	361	ACTGAAGACAGATPACTAGTAATAATTTGGAGAACTTAAAAATTTTTT-----	408
Qy	155	IleGlnArgIleThrCysProAsnValAlaPdeLysTyrPheProSerSerValLysProThr	174
Db	409	-----CAGATPACTGTGAAAC-----AGTTACATCAAAACACGTGTCAACAGACA	456
Qy	175	IleThrTyrTyrMetGlyCysTyrLysIleGlnAsnPheAsnValIleProGlu--	193
Db	457	---TCATTGTATTAAGAACTGTAAAAAGCTACTACTGAGAAACAATAAAACCCAAACATA	513
Qy	194	GlyMetAsnLeuSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrTrpCysVal	213
Db	514	AAGAAAGAACCGCAGATT-----GAAAGTAGGGGTAATTACTCTCTGGTG	558
Qy	214	ValThrTyrProGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysVal	233
Db	559	CATTTCCTTCACTAATAGAAAACATTTAATATTCACCAAAACCTTCATATATACATA	618
Qy	234	ValGlySerProLysAsnAlaValProProValIleHisSerProAsnAspHisValVal	253

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Db      619 GTGGAATCGCAGTAAATATAGTTCGGTTCCTTGACACCAACCTTAACCATGTGCA 678
Oy      254 TTTGTLuysGLuProGluYGLuGLuLeuLeuLleProCyThValTyRheSerPheLeu 273
Db      679 GTGGAATTA-----GGAAAAAGTAAGGCTCACTG-----CTGCTTG 720
Oy      274 MetAspSerArgAngluValLTPTrPThrLleAspGlyLyAsLyArgProAspLleThr 293
Db      721 CTGAATGAAGAGATGTAATTATTGTGATGTTCCGGGAAGAAAATGATCGGATCTTAAT 780
Oy      294 LLeAspValThrLleAngluSerLleSerHisSerArgThrGluAspGluThrArgThr 313
Db      781 ATA-----CATGAAGAGAAAAGAAATGAGAAATTAGTATGACT 813
Oy      314 -----GlnLleLeuSerLleLyAsLyValThrSerGluAsp 325
Db      814 CCAGAGGCAAAATGCGACTCTTCAAAAGTAATGAGAAATGAAATAATGTGTGAAGCAAT 873
Oy      326 LeuLyAsArgSerTyValCySHleAlaArgSerAlaLyGlyGluValAlaLeysAlaLa 345
Db      874 CTAAATGTTTATTAATTAATGCACTGTGGCAGCAGGAGGACACACCAAAAGCTTC 933
Oy      346 LysValLysGlnLys-----ValProAlaProArgTyThrValGluLeuAla 361
Db      934 ATCTGTGGAGAAAAGACATGGCTGATATCCAGGCAAGCTTGACA----- 981
Oy      362 CysGlyPheGlyAlaThrValLeuLeu-----ValValLleLeuLleValValTyR 378
Db      982 AGAGAGATGATCATACGCTGTGTGATCTGTGGCAGTGTGATGCTGATGATGATGCTGT 1044
Oy      379 HisValTyRTrpLeuGluMetValLeuPheTyRArgAlaHisPheGlyThrAspGluThr 398
Db      1042 GTCAATTATTAAGAGTGACTGTGTTCTTAATTTTAAGACATTTAAACGAAAGAAATGAACA 1101
Oy      399 LLeuAspGlyLysGluTyRAspLleTyRValSerTyRAlaArg----- 413
Db      1102 TTACAGATGAAAAAATAATGATGCTTTGTGTCTTACTTAAAGAAATGCCAGACTGAA 1166
Oy      414 AsnAlaGluGluGluPheValLeuLeuThrLeuArgGlyValLeuGluAsnGluPhe 433
Db      1162 AATGAGAGGAGGACACACTTGTGCTGTGAGATTTTCCAGAGGTTGTGAGAAACATTTT 1221
Oy      434 GlyTyRtyrLeuCySHlePheAspArgAsnSerLeuProGlyGlyAsnThrValGluAla 453
Db      1222 GGGTATTAAGTATATGCAATTTTGAAGAGAGTAAGTGTCCGTGAGAGAGCTTTGTATGAA 1281
Oy      454 ValPheAspPheLleGlnArgSerArgArgMetLleValValLeuSerProAspTyRVal 473
Db      1282 ATCCACTCACGATGAGAAAAGCCAAAGACATATATCTCTTAAGTAAAGATTATAG 1344
Oy      474 ThrGluLysSerLleSerMetLeuGluPheLySleu--GlyValMetCysGlnAsnSer 492
Db      1342 TCTAATGAGGTCAGGTAATGAACTTGAAGAAGGACCTCATGAAGCAATTTGGTGAAGAAA 1401
Oy      493 LLeAlaThrLySleuLleValValGluTyRArgProLeuGluHisProHis-----Pro 510
Db      1402 ATT-----AAATAAATCTTAATTTGAATTTAACCCCTTACTGACTTCACATCTTGCCC 1455
Oy      511 GlyLleLeuLeuLysGluSerValSerPheValSerTyRProGlyGlyLysSerLyS 530
Db      1456 CAATCATCAAGCTTTGAAATCTCACACAGATTTGAAGAGGAAGCCATTAATCTCTT 1511
Oy      531 HisSerGlySerLySPheTrpLySAlaLeuArgGluAlaLeuProLeuAspArgSerLeu 549
Db      1516 TCTTATTACTCAAGCTTCTGGAAGAACCTTCTTACTTAATATGCTGCAAAAACAGTC 1572

RESULT 7
US-08-604-333-1
; Sequence 1, Application US/08604333
; Patent No. 576731
; GENERAL INFORMATION:
; APPLICANT: Parmet, Patricia et al.
; TITLE OF INVENTION: Receptor Designated 2P1

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```

NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/604.333
FILING DATE: 21-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2619
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1626 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: hu2f1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1626
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 58..1623
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1..57
US-08-604-333-1

Alignment Scores:
      8.48e-45      Length: 1626
      528.00       Matches: 174
      46.03%      Conservative: 93
      30.00%      Mismatches: 215
      14.39%      Indels: 98
      1         Gaps: 27
      1         DB: 27

US-10-061-727-2 (1-687) x US-08-604-333-1 (1-1626)
QY 4 LeuTPGyValValSerLeuTYrPheTYrGlyIleLeuGlnSerAspAlaSerGluArg 23
DB 28 CTTTGGGTCCTTATATCTGTA-----AGCACTGCAGAACTCT 63
QY 24 CysAspAspTrpGlyLeuAspThrMetArg---GlnIleGlnValPheGlnAspGluPro 42
DB 64 TGT-----ACTTCACTCCCACTTACTGTGTTGAAGCGAACT 105
QY 43 AlaArgIleLys---CysProLeuPheGlnHisPheLeuLysPheAsnTYrSerThrAla 61
DB 106 TTTCTATCTGAACATTCG-----TCGTTTCACTTGCA 138
QY 62 HisSerAlaGlyLeuThrIleu---IleTrpTYrTrpThrArgGlnAspArgAspLeuGlu 80
DB 139 CATTGACATTGAACACACCAAAAGCTGGTACAAAAGAGTGATCAGCAATGTG 198

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QY 81 GlnProIleAsnPheArgLeuProGlnAsnArgIleSerLysGlnLysAspValLeuTrp 100
DB 199 GAG---CTGAACCCAG---AGTTCTCGAAGATTCCTTGTCATGATGTTGTTGGAG 252
QY 101 PheArgProThrIleLeuAsnAspThrGlyAsnTYrThrCysMetLeuArgAsnThr 120
DB 253 TTTGGCCAGTTGAGTTGAATGACACAGATCTTACTTTTCCAAATATAATATATCT 312
QY 121 TYrCysSerLysValAlaPheProLeuGlnValValGln-----LysAspSerCysPhe 138
DB 313 CAG-----AAATGAAATTAATGTCATCAGAAAGAAATTAACACAGCTGTTTC 360
QY 139 Asn-----SerProMetLysLeuProValHisLysLeuTYrIleGluTYrGly 154
DB 361 ACTGAAGACAGTACTAGTAAATGTGCAAGTTAAATAATTTTT-----408
QY 155 IleGlnArgIleThrCysProAsnValAspGlyTYrPheProSerSerValLysProThr 174
DB 409 -----CAGATTAACCTGTGAAC-----AGTTACTATCAAAACCTGCTCAACAGCA 456
QY 175 IleThrTrpTYrMetGlyCysTYrLysIleGlnAsnPheAsnAsnValIleProGlu--- 193
DB 457 ---TCATTGTATTAAGACTGTAAAGAGCTACTCGAGAACATTAATAACCAACGATA 513
QY 194 GlyMetAsnLeuSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTYrThrCysVal 213
DB 514 AAGAAGACGCCGAGTTT-----GAAGATCAGGGGTATTAATCTCGCGTG 558
QY 214 ValThrTYrProGlnAsnGlyArgThrPheHisLeuThrArgThrLeuThrValIleVal 233
DB 559 CATTCTCTTCATCATATGAGAAACATATTATATACCAAAACCTTCATATTAACATA 618
QY 234 ValGlySerProLysAsnAlaValProProValIleHisSerProAsnAspHisValVal 253
DB 619 GTGGAAGATCGAGTAATATATGTTCCGTTCTTTCGACCAAACTTAACATGTTGCA 678
QY 254 TYrGlnLysGlnProGlyGlnGlnLeuLeuIleProCysThrValTYrPheSerPheLeu 273
DB 679 GTGGAATTA-----GGAAGAAAGTAAAGCTCAACTGC-----TCTGCTTG 720
QY 274 MetAspSerArgAsnGlnValTrpTrpThrIleAspGlyLysLysProAspAspIleThr 293
DB 721 CTGAATGAGAGATGTATATATGATGATGTTGGGAGAAATGATCGATCTTAAT 780
QY 294 IleAspValThrIleAsnGlnSerIleSerHisSerArgThrGlnAspGluThrArgThr 313
DB 781 ATA-----CATGAAGAGAAAGAAATGAATTAATGACT 813
QY 314 -----GlnIleLeuSerIleLysLysValThrSerGlnAsp 325
DB 814 CCAGAAAGCAATATGCAATCTTCAAAAGATTTGAGAAATTAATGCTGAAAGCAAT 873
QY 326 LeuLysArgSerTYrValCysHisAlaArgSerAlaLysGlyGlnValAlaLysAlaAla 345
DB 874 CTAAATGTTTATATATATATGCACTGTGGCCACGACGAGACAGACACCAAAAGCTTC 933
QY 346 LysValLysGlnLys-----ValProAlaProArgTYrThrValGlnLeu 360
DB 934 ATCTTGTCAGAAAGAGACAGACATGCTGATATCCAGGCCAGCTTTCACA-----984
QY 361 AlaCysGlyPheGlyAlaThrValLeuLeu-----ValValIleLeuIleValVal 377
DB 985 ---AGAGAAATGATCATATGCTGTTTGAATCTTGTCGAGAGATGTGCTAGTACTG 1041
QY 378 TYrHisValTYrTrpLeuGlnMetValLeuPheTYrArgAlaHisPheGlyThrArgGlu 397
DB 1042 TGTGTCATTATAGAGTGAATGCTATGTTCTTATTTATAGCAATTAAAGAGAGATGA 1101
QY 398 ThrIleLeuAspGlyLysGlnLysValSerTYrValArg-----413
DB 1102 ACATTTAACAGATGGAAGAAACATATATGCTTTGTGCTTACCTTAAGAAAGCCGACT 1161
QY 414 ---AsnAlaGlnGlnGlnGlnLeuValLeuThrLeuArgGlyValLeuGlnAsnGlu 432

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Db 1162 GAAATGAGAGAGACACCTTCTGTGAGATTTTCCAGAGGTTGGAGAAACAT 1221
Qy 433 PheGlyTyrTyrLeuValIlePheAspArgSerLeuProGlyValAsnThrValGlu 452
Db 1222 TTTGGGTATAGTATCATATTTTGAAGAGATTTAGCTTGGAGAGAGCTTTGTGAT 1281
Qy 453 AlValPheAspPheIleGlnSerArgArgMetIleValIleLeuSerProAspTyr 472
Db 1282 GAATTCACCTCAGTATGAGAAAGCCGAAAGCTATCATCTTGTCCCTTAAGAAAGTAT 1341
Qy 473 ValThrGlySerIleSerMetLeuGluPheLeu---GlyValMetCysGlnAsn 491
Db 1342 ATGCTATAGTACGATGATGAGTGAAGTGAAGTGCATGCAAGCATTTGGTGAAGA 1401
Qy 492 SerIleAlaThrIleValIleValGluTyrArgProLeuGluHisProHis----- 509
Db 1402 AAAATT-----AAAATAATCTTAATTAATTAACCTGTACTGACCTTCACATTTCTG 1455
Qy 510 ProGlyIleLeuGlnLeuValSerValSerPheValSerThrIleGlyValSer 529
Db 1456 CCCCAATCATTAAAGCTTTGAATCTCACAGAGTTCGAAGTGAAGCCGATTAATCT 1515
Qy 530 LysHisSerGlySerIlePheTyrPheValLeuArgLeuAlaLeuProLeuArgSerLeu 549
Db 1516 CTTTCTTATTAATCAAGTCTCTGGAAGACCTTCTTACTTAATGCTTGAAGAAACAGTC 1575
RESULT 8
US-09-110-618-1
Sequence 1, Application US/09110618
Patent No. 6090918
GENERAL INFORMATION:
APPLICANT: Parnet, Patricia et al.
TITLE OF INVENTION: Receptor Designated 2F1
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/110,618
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/604,333
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2619
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1626 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: hu2F1

FEATURE:
NAME/KEY: CDS
LOCATION: 1..1626
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 58..1623
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1..57
US-09-110-618-1
Alignment Scores:
Pred. No.: 8,48e-45 Length: 1626
Score: 528.00 Matches: 174
Percent Similarity: 46.03 Conservative: 93
Best Local Similarity: 30.00 Mismatches: 215
Query Match: 14,398 Indels: 98
Gaps: 27
US-10-061-727-2 (1-687) x US-09-110-618-1 (1-1626)
Qy 4 LeuThrCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAlaSerGluArg 23
Db 28 CTTTGGGTGCTTATATCTGTA-----AGCACTGCAGAAATCT 63
Qy 24 CysAspAspThrGlyLeuAspThrMetArg---GlnIleGlnValPheGluAspGluPro 42
Db 64 TGT-----ACTTACGTCCTCCACATTACTGTGTGAAGGGAACCT 105
Qy 43 AlaArgIleLys---CysProLeuPheGluHisPheLeuLysPheAsnTyrSerThrAla 61
Db 106 TTCTATCTGAACAATCTGC-----TCGTGTCACTTGCA 138
Qy 62 HisSerAlaGlyLeuThrLeu---IleTyrTyrThrArgGlnAspArgAspLeuGlu 80
Db 139 CATGAGATTGAAACCAACCAAGAGCTGTACAAAGCAGTGCATGACGAAGAACATGTG 198
Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTyr 100
Db 199 GAG---CTGAACCAAGG---AGTTCCTCGAAGATTCCTTGCATGATGTGTTTGAG 252
Qy 101 PheArgProThrIleLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Db 253 TTTTGGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 312
Qy 121 TyrCysSerLysValAlaPheProLeuGluValGln-----LysAspSerCysPhe 138
Db 313 CAG-----AAATGAATTAATTAATGATCATGAGAAATTAACACAGCTGTTTC 360
Qy 139 Asn-----SerProMetLysLeuProValHisLysLeuTyrIleGluTyrGly 154
Db 361 ACTGAAGAAGACAGTAACTAATAAATTTGGAAGTTAAATTTT-----408
Qy 155 IleGlnArgIleThrCysProAsnValAspGlyTyrPheProSerSerValLysProThr 174
Db 409 -----CAGATTAACCTGTGAAGC-----AGTTACATCAACACAGCTGCAACAGACA 456
Qy 175 IleThrTyrTyrMetGlyCysTyrLysIleGlnAsnPheAsnValIleProGlu---193
Db 457 ---TCATTTATTAAGAACTGTAAGAAAGCTACTCTGAGAGAAATTAACCAACAGATA 513
Qy 194 GlyMetAsnLeuSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysVal 213
Db 514 AAGAGAAGCCGAGATT-----GAAATCAAGGGATTAATCTCTCGGTG 558
Qy 214 ValThrTyrProGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValVal 233
Db 559 CATTTCTTATCATATATGAGAAAGTATTAATATATCAACCAACCTTCATATATACATA 618
Qy 234 ValGlySerProLysAsnAlaValProProValIleHisSerProAsnAspHisValVal 253
Db 619 GTGGAAGATGACAGTATATATAGTTCCGTTCTTCTGGAACCAAGCTTAACATGATGCA 678

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Qy 254 TyrGluysgluProgluGluLeuileProCysThrValTyrPheSerPheLeu 273
Db 679 CTGGAATTA-----GAAAAGAGTGAAGCTCAACTC-----TCGCTTG 720
Qy 274 MetAspSerArgangluValTyrThrIleAspGlyLysProAspAspIleThr 293
Db 721 CTGAATGAAAGAGATGTAATTAATGATGTTGGGAGAAAGATCGATCTTAAT 780
Qy 294 IleAspValThrIleangluSerIleSerIleSerArgThrGluAspGluThr 313
Db 781 ATA-----CATGAGAGAAAGAAATGAGATTAATGACT 813
Qy 314 -----GlnIleuSerIleLysValThrSerGluAsp 325
Db 814 CCAGAGGCAAAATGCGATCTTCAAAGATTTGAGATTGAAATATTGGTGAAGCAAT 873
Qy 326 LeuLysArgSerTyrValCysHlaIaArgSerAlaLysGluValAlaLysAla 345
Db 874 CTAATGTTTATATATTAATGACATGCGCAGACGGAGGACAGACACCAAAAGCTTC 933
Qy 346 LysValLysGlnLys-----ValProAlaProArgTyrThrValGluLeu 360
Db 934 ATCTTGAGAGAAAAGCAGACATGCGTGAATCCAGGCCACGCTTCACA----- 984
Qy 361 AlaCysGlyPheGlyAlaThrValLeuLeu-----ValValIleLeuIleVal 377
Db 985 ---AGAGATGATCATATGCTGTTTATCTTGGTGGCAGATGAGTGCTTGAATCTG 1041
Qy 378 TyrHisValTyrTyrLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGlu 397
Db 1042 TGTGTCAATTATAGAGTTGACATGCTGTTATTTATAGACATTAACAGAAAGATGAA 1101
Qy 398 ThrIleLeuAspGlyLysGlnTyrAspIleTyrValSerTyrAlaArg----- 413
Db 1102 ACATTAAACAGATGAGAAAACATATATGCTTGTGCTTAACTTAAGAAAGTCCGACT 1161
Qy 414 ---AsnIaGluGluGluGluPheValLeuLeuThrLeuArgGlyValLeuGluAsnGlu 432
Db 1162 GAAATGAGAGAGAGACACACCTTGTCTGTGAGATTTGCCAGGGGTGTGAGAAACAT 1221
Qy 433 PheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGlyLysAsnThrValGlu 452
Db 1222 TTGGGTATATAGATTATGATATTTGAAGGATGATGCTGAGAGAGCTGTTGAT 1281
Qy 453 AlaValPheAspPheIleGluArgSerArgArgMetIleValValLeuSerProAspTyr 472
Db 1282 GAAATCCATCATGATGAGAAAGCCGAAAGCACTAATCATTTGCTTAAGTAAAGTTAT 1341
Qy 473 ValThrGluLysSerIleSerMetLeuGluPheLysLeu---GlyValMetCysGluAsn 491
Db 1342 ATGCTAATGAGGTGAGTATGAACTTGAAGTGAATTCCTCAAGAACATTTGTGGAAGA 1401
Qy 492 SerIleAlaThrLysLeuIleValValGluTyrArgProLeuGluHisProHis----- 509
Db 1402 AAAATTT-----AAATATATCTTAATGATTAACACTGTTAGCACTTCACTTCG 1455
Qy 510 ProGlyIleLeuGluLeuLysGluSerValSerPheValSerTyrPheGlyGluLysSer 529
Db 1456 CCCCAATCACTAAAGCTTTTAAATCTTCACAGAGTTTGAAGTGAAGCCGCAATTAATCT 1515
Qy 530 LysHisSerGlySerLysPheTyrPheLysAlaLeuArgLeuAlaLeuProLeuArgSerLeu 549
Db 1516 CTTTCTTAATCACTCAAGGTTCTGAAGAACCTTTCTTAATATGCTTCGAAACAGTCT 1575

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ADDRESSER: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/578,178
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/110,618
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2619
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1626 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: hu2F1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1626
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 58..1623
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1..57
US-09-578-178-1
Alignment Scores:
Pred. No.: 8,48e-45 Length: 1626
Score: 528.00 Matches: 174
Percent Similarity: 46.03% Conservative: 93
Best Local Similarity: 30.00% Mismatch: 215
Query Match: 14.39% Indels: 98
DB: 4 Gaps: 27
US-10-061-727-2 (1-687) x US-09-578-178-1 (1-1626)
Qy 4 LeuTyrCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAlaSerGluArg 23
Db 28 CTTGGGTGCTTAATATCTGA-----AGCACTGACAGATCT 63
Qy 24 CysAspAspTyrPheLysLeuAspThrMetArg---GlnIleGlnValPheGluAspGluPro 42
Db 64 TGT-----ACTTCACGTCCTCCACACATTAATCTGTGTTGAAGGAGAACT 105
Qy 43 AlaArgIleLys---CysProLeuPheGluHisPheLeuLysPheAsnTyrSerThrAla 61
Db 106 TTTATCTGAACATTCG-----TCGCTTCACTTGA 138
Qy 62 HisSerAlaGlyLeuThrLeu---IleTyrTyrThrArgGlnAspArgAspLeuGlu 80
Db 139 CATGAGTTGAACACCAACCAACCAAGCTGTACAAAGACAGTGCATCAGAGAACATG 198

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; STRADEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: 1..1563
; IDENTIFICATION METHOD:
;
US-08-996-338-1

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Alignment Scores:	
Pred. No.:	5,36e-44
Score:	520.00
Percent Similarity:	46.80%
Best local Similarity:	30.53%
Query Match:	14,17%
DB:	3
Gaps:	24
Length:	156
Matches:	167
Conservative:	89
Mismatches:	209
Indels:	82
Gaps:	24

US-10-061-727-2 (1-687) x US-08-996-338-1 (1-1563)

35 IleglnvalPhegluaSpgluProalarglleys---CysProleuPhegluHlsPhe 53
 25 ATTACTGGTGTGAAGGGGAACCTTTCTATCTGAACAATTGC----- 66
 54 LeuylsPheasnTySerThralHisSerzlaGlyleuThrlleu---lletPrTyTrp 72
 67 -----TCGTCTTCACTTGACACATCAAGTTGAACACACCAACCAACTGTCACAA 117
 73 ThrArglnAspArgAspLeuGlulgluProlleasnPheArgleuProgluaenArglle 92
 118 AGCAGTGTGATCAGGACGACATGTGGAG---CTGAACCCAAAGS---AGTTCCTCGAAGATT 171
 93 SerlySglulysAspValleuTrpPheArgProThrlleuLeuIsnAspTrnglyasnTy 112
 172 GCTTTCGATGATTGTGTTTGGAGTTTGGCGAGTGAAGTTGAATGCACAGAGACTTCA 231
 113 ThrCysmetLeuArgasnThrThTyrcCysSerlySvalAlaPheProleuGlulVal 132
 232 TTTTTCCAATGAAATAATTAATACCTCAG-----AAATGAAATTAATATGTCATC 279
 133 Glu-----LysAspSerCysPheasn-----SerPrometlySleuProval 146
 280 AGAAGAAATTAACACACAGCGCTTTCACTGAAGACAGATTAAGTAATTAATTTGGAAATT 339
 147 HislySleuTyrlleGluTyrellylleglnArglleThrcysProleuValAspGlyTy 166
 340 AAAAAAATTTTT-----CAGATTAACCTGTGAAAC-----AGTTAC 375
 167 PheProSerSerVallySProThrlleThTrpTyMetGlyCysTyrllySllleglnAsn 186
 376 TATCAAAACCTGCTCAACAGCACA---TCATTGTATTAAGAACTTAATAAGCTTACTG 432
 187 PheasnValilleProglu---GlyMeAsnleuSerPheleuilealaleuIleSer 205
 433 GAGAACATTAATAAACCAACAGATTAAGAAGAACCCGACAGTT-----GAA 477
 206 AsnaSnglyasnTyTrhCysValValThrTyTrpProgluaSnglyArgThrPheHlsleu 225
 478 GATCAGGGGTATTACTCCGCGCTGATTTCTTCATCATTAAGAAAACATTAATTAATAC 537
 226 ThrArgThleuThVallySValValGelySerProlySaamAlaValProProvalille 245
 538 ACCAAAACCTTCAMATATACATATGTGGAAGATCGCACTAATATAGTCCGGTCTTCTT 597
 246 HisSerProasnAspHisValValTyrglySgluProgllyGlulgluIleuIlePro 265
 598 GGAACCAAGCTTAACCATTTGTCAGTGAATTA-----GAAAAAACGTAAAGGCTCAAC 651
 266 CysThValTyPheSerPheleuMetAspSerArgAsngluValTrpTrpThrlleasp 285
 652 TGC-----TCTGCTTTCGTGAATGAAGAGATTAATTAATTTGATGATGTCGGG 699
 286 GlylySlySProleAspIleThrlleAspValThrlleamgluSerIleSerHisSer 305

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Db      700  GAGAAAGAAATGAGATCGATCCAAATATAT-----CATGAA  732
Qy      306  ArgThrGluSerGluThrArgThr-----GlnIleLeuSer  317
          |||
Db      733  GAGAAAGAAATGAGAAATTAATATATATCCAGAAAGCAAAATGCGATGCTTCACAAAGTAATGAGA  792
Qy      318  IleLysLysValIThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAla  337
          |||:::
Db      793  ATTGAAATATATGTGTGAAGCAATCTAAATGTTTATATATATATGACATGTCGGCCAGACAG  852
Qy      338  LysGluGluValAlaLysAlaLysValLysGlnLys-----ValProAla  353
          |||
Db      853  GGAGGCACACAGCACCCAAAGCTTCATCTTGGTGAGAAAGAACATGCGTGAATATCCAGGC  912
Qy      354  ProArgTyrThrValGluLeuAlaCysGlyPheGlyAlaThrValIleLeu-----  370
          ::::|
Db      913  CACGCTTCACAC-----AGAGAAATGATCATACAGCTGTTTGAATCTTGCGTGGCA  960
Qy      371  ValValIleLeuIleValValTyrHisValTyrTrpLeuGlnMetValIleuPheTyrArg  390
          |||:::
Db      961  GTAAGTGTCCATGACATCTGTGTGTGTGCATTTATAGAGTGTGACTTGCTTGTTATATATAGA  1020
Qy      391  AlaHisPheGlyThrAspGluThrIleLeuAspGlyLysGluTyrAspIleTyrValSer  410
Db      1021  CATTTAAGCAGAGAGATGAAACATTAACACATGACATGAAAGAAACATATGATGCTTTGTGTCT  1080
Qy      411  TyrAlaArg-----AsnAlaGluGluGluGluPheValIleuLeuThrLeu  425
          |||:::
Db      1081  TACCTAAAGAAATGCCACCTGAAATATGAGAGAGACACCTTGCTGTGGAGATTTTG  1140
Qy      426  ArgGlyValIleuGluAsnGluPheGlyTyrTyrLysLeuCysIlePheAspArgAspSerLeu  445
          |||
Db      1141  CCCAGGCGTGTGGAGAAACATTTTGGGTATAGTTATGCAATTTATGAAAGGATGTAGTG  1200
Qy      446  ProGlyValAsnThrValGluAlaValPheAspPheIleGlnIleArgSerArgArgMetIle  465
Db      1201  CCGTGAAGAGCTGTGTGTGTAAGAAATCCACATCCTGATAGAGAAAGCCGAAAGATTAATC  1260
Qy      466  ValValIleuSerProAspTyrValThrGluLysSerIleSerMetLeuGluPheLysLeu  485
          |||
Db      1261  ATTTGCTTAAGTAAAGTATATATATGCTAAATAGAGTCAAGGTATGAACCTTGAAGATGACCT  1320
Qy      486  ---GlyValMetCysGlnAsnSerIleAlaThrLysLeuIleValGluTyrArgPro  504
          :::
Db      1321  CATGAAGCATTTGGTGAAGAAAGAAATTT-----AAATATATCTTAATGAATTAACACT  1374
Qy      505  LeuGluHisProHis-----ProGlyIleLeuGlnLeuLysGluSerValSerPheVal  522
          ::::|
Db      1375  GTTACTGACTTCACATCTTGTCGCCAATCCATCAATAGCTTTTGAAATCTCACAGACTTGTG  1434
Qy      523  SerTyrLysGlyLysSerLysHisSerLysSerLysPheTyrLysAlaLeuArgLeu  542
          |||
Db      1435  AAGTGAAGGCCGATTAATCTCTTCTTAACTAATCAAGGTTCTGGAAGAACCTTCTTAC  1494
Qy      543  AlaLeuProLeuArgSerLeu  549
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Db      1495  TTAATGCTGCAAAACACAGTC  1515

RESULT 11
US-09-173-151A-9
: Sequence 9, Application US/09173151A
: Patent No. 6326472
: GENERAL INFORMATION:
: APPLICANT: Timans, Jacqueline C.
: APPLICANT: Debets, Johannes Eduard Maria
: APPLICANT: Antonius
: APPLICANT: Sana, Theodore R.
: APPLICANT: Bazan, J. Fernando
: APPLICANT: Kasteleijn, Robert A.
: TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
: NUMBER OF SEQUENCES: 36
: CORRESPONDENCE ADDRESS:
: ADDRESS: DNAX Research Institute

```

STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,151A
FILING DATE: 14-OCT-1998
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2314 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 109..1905
US-09-173-151A-9

Alignment Scores:
Pred. No.: 4,18e-41 Length: 2314
Score: 495.00 Matches: 181
Percent Similarity: 44.25% Conservative: 127
Best Local Similarity: 26.01% Mismatches: 288
Query Match: 13.49% Indels: 104
DB: 4 Gaps: 27

US-10-061-727-2 (1-687) x US-09-173-151A-9 (1-2314)

QY 11 TyrPheTyrGlyLeuGlnSerAspAlaSerGluArgCysAspAspTrpGlyLeuAsp 30
DB 128 TATTTCCTTGGCTTGTGACGGA-GAGCGAATTAAAGATTAAATTTCAGGTGTTCC 186
QY 31 ThMetGrgInIleGlnValPhe-----GluAspGluProAlaArgIleGlyCys 47
DB 187 ACAGAAAAACCTCTTGACATATTCTACAGAGAGAGAGAAATTGTCTTATTGT 246
QY 48 ProlenPheGlu-----HisPhe----- 53
DB 247 GATTACACAGACGACAGAAATCATATTCTGACAGAAATGACACTCTACCAAAACAA 306

QY 54 -----LeuLysPheAsnTyrSerThrAlaHisSerAlaGlyLeuThrLeuIle 69
DB 307 GTCCCTGACACCTGCCCTTCATGGGTAGTAACGACTTACT-----GATGCCAA 357
QY 70 TrpTyrTrpThrArgGlnAspArgLeuGluGlnProIleAsnPheArgLeuProGlu 89
DB 358 TGGTACCACCAACCTTCGATGAGATCCATTAGAGACATTAGAGAAAGCTATCTCT 414
QY 90 AsnArgIleSerLysGlnLysAspValLeuTrpPheArgProThrLeuLeuAsnAspThr 109
DB 415 ---CAATCTTCAGACCAAAATGACTCTTACCTTTTACACCCAGGGGTGAATATTCT 471
QY 110 GlyAsnTyrThrCys-----MetLeuArg-----AsnThrThrTyrCysSer 123
DB 472 GGGTCATATATTGTGACACCAAGATGATTAAAGACCCCTGATGATGACTGTGTGTC 531
QY 124 LysValAlaPheProLeuGlnValValGlnLysAspSerCysPheAsnSerProMetLys 143
DB 532 AAGATGATTTAGAGATGAGCCCAAGCAAAATGCAATCTGTGAGATTCGCCATCA 588
QY 144 LeuProValHisLysLeuTyrIleGluTyrGly-----IleGlnArgIleThrCysProAsn 162
DB 589 -----CATAGCAAGACCTACTCTTGGAGACACTGGCTCTATTCTTCCCCAGT 639
QY 163 ValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly----- 180
DB 640 CTCAGCGCCCA---AGTATGACCAAAAGTCCAGCGGTAACTCGTACCAAGATGAGAA 696
QY 181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetCysLeuSerPheLeu 200
DB 697 CTCCTCTCTGTGGAAGAGCAACCGAATCGTAGCGAAGTT----- 741
QY 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValIleThrTyrProGluAsnGly 220
DB 742 -----TATGACTATACCAAGGACATATGATGATTACTACTAGTCGATCTGTC 795
QY 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
DB 796 AGTTCGACGACACTCAGAGCTGTGTTCAGATGAGAACCATTTGTGGAGACACTAAACTC 855
QY 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
DB 856 AAACCAATATCTCGATCTCGATCTCGAGGAC-----ACACTGGAAGTACCACTTGGAAG 909
QY 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetCysAspSerArgAsnGluVal 280
DB 910 CTTTAACTATTAGCTCAAGACGATTTGCTTGAAGGCTCTTAACTGTACATA 969
QY 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
DB 970 AATGTGATCATC-----AAAGATCTGACCTGAGTGGAACTCATGACTGAG 1020
QY 301 SerIleSer---HisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLys 319
DB 1021 GCGAAAGATTTAAATCCACTTTAAAGATGAATATGAGGTAAATATCTTGGA 1080
QY 320 LysValIleHisSerLysLeuLysAspSerTyrValCysHisAlaArgSerAlaLysGly 339
DB 1081 AAGTCACTCAGCGGTATCTTCGACAGAAAGTTGTGCTTGTCCAGAACTCATTTGA 1140
QY 340 GluValAlaLysValAlaLysValLysGlnLysValProAlaProArgTyrThrValGlu 359
DB 1141 AACCAACCAACGTCCTGCAACTGAAAGAAAG-----AGAGAGTGTGCTC 1188
QY 360 LeuAlaCysGlyPheGlyAlaThrValLeuLeuValValIleLeuIle-----ValVal 377
DB 1189 CTGATCATCTGTGCTGGACCAATCGGACCTGTGTGCGGTGCGGCGAGTGCCTTC 1248
QY 378 TyrHisValTyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGlu 397
DB 1249 CTCACAGGACATGATGAATATGATGCTGCTGTACCGGACCTACCAAGCAAGCAAGATCAG 1308
QY 398 ThrIleLeuAspGlyLysGluTyrAspIleTyrValIleSerTyrAlaArg----- 413

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Db 1309 ACCGTTGGGATTAATAAGATTTGATGCTTGTATCTATGCAATAAGAGCTCTTTT 1368
Qy 414 -----AanAlaGlugluGluGluPheValleuThrlauArgGly 427
Db 1369 CCAAGTGAAGCCACTTATCTCTGAGTGAAGAACACTTGGCCCTGAGCCCTATTTCCTGAT 1428
Qy 428 ValleuGluGluGluPheGlyTyrLysLeuGlyLysPheAspArgAspSerLeuProGly 447
Db 1429 GTTTTGAATAAATAATGATATAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGGA 1488
Qy 448 GlyAsnThrValGluAlaValPheAspPheLeuArgSerArgGlyMetLeuVal 467
Db 1489 GGAGTGTATGCAAGACATTTGACATTTATTAAGAGAACAGAACAGAAATATTATC 1548
Qy 468 LeuSerProAspTyrValThrGluLysSerLysSerMetLeuPheLysLeuGlyVal 487
Db 1549 TTATGCCCCCACTATGATCAATGACCCAGCACTTGTATTAAGTCTGTATCTTCCAGAG 1608
Qy 488 MetCysGlnAsnSerLeuAlaThrLysLeuLysValValGluTyr-----Arg 503
Db 1609 GCCTTGATGATCAAA--ACACTGAAATCATTTTATTAAGTCTGTATCTTCCAGAG 1665
Qy 504 ProLeuGluHisProHisProGlyLysLeuGluLeuLysLeuValSerPheValSer 523
Db 1666 CCAGAGCTCTTACTCATCTC--GTGAAAAAAGCTCTCAGGCTTTTGCACAGTACT 1722
Qy 524 TrpLysGluGluLysSerLysHisSerGlySerLysPheThrLysAlaLeuArgLeuAla 543
Db 1723 TGAAGAGGCTTAATAATCACTTCTCCCAATTTAGGTTGTGGCCAAATGCGCTACAC 1782
Qy 544 LeuProLeuArgSerLeuSerLysSerGlyTyrAsnGluSerCysSerSerGlnSer 563
Db 1783 ATGCTGTGAAAAAC--TCTCAGGATTCACCTGAGAACAGCAGCAGCAATTAATCTAG- 1838
Qy 564 AspLysSerLeuAspHisValGlnArgArgSerArgLysLeuLysProProGluLeu 583
Db 1839 GATTTTCACTGAGAAAGACTCAGTAGAACAGAACACACGAGGAGCT-CCAGGCTA 1897
Qy 584 GlnSerSerGluArgAlaAlaGlySerPro-----ProAlaGly***MetSerLys 601
Db 1898 AGCAATGCTGAATGAGCCCTGAGGCCCTCCAGTCCAGTCCCTGCG--ATAAGAGATG 1954
Qy 602 HisArgGlyLysSerSerAlaThrCysArgCysValThrTyrCysGluGlyGluAsn 621
Db 1955 TT-GCTGACAGAACTCAGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTC- 1992
Qy 622 HisLeuArgAsnLysSerArgAlaGluLysHisAsnGlnProGlnThrHisLeu 641
Db 1993 AGGCTATAGCAAAATTCAAAGAGCTCTCTG----- 2022
Qy 642 CysLysProValProGlnGluSerGluThrGlnThrLysGlnAsnGly 657
Db 2023 -----CCAGCACCAAGCAAGCTTGTATGCAATAG-----AATGGG 2058

RESULT 12
; Sequence 3, Application US/07821716
; Patent No. 5119071
; GENERAL INFORMATION:
; APPLICANT: Dower, Steven K.
; APPLICANT: March, Carl J.
; APPLICANT: Sims, John
; APPLICANT: Urdal, David L.
; TITLE OF INVENTION: Soluble Interleukin-1 Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
```

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/821,716
FILING DATE: 19920114
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 125627
FILING DATE: 25-NOV-1987
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 160550
FILING DATE: 25-FEB-1988
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 258756
FILING DATE: 13-OCT-1988
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 691551
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wight, Christopher L.
REGISTRATION/DOCKET NUMBER: 31,680
REFERENCE/DOCKET NUMBER: 2001-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 587-0606
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2356 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mouse
IMMEDIATE SOURCE:
LIBRARY: M01L1R
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1955
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 282..1952
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 225..281
US-07-821-716-3
Alignment Scores:
Pred. No.: 2,04e-40 Length: 2356
Score: 488.50 Matches: 175
Percent Similarity: 43.21% Conservative: 121
Best Local Similarity: 25.55% Mismatches: 254
Query Match: 13.31% Indels: 136
Gaps: 31
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Db 285 GAGATTGACGTATGTCACAAATATCAATCAATGCTTTTGTATCTGTAATGAA 344
Qy 46 -----LysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThrAla 61
Db 345 ATTGATATTGCAAGTGTCTCTTACTCCAAATAAATGAC----- 386
Qy 62 HisSerAlaGlyLeuThrLeuLysTyrTyrThrArgGlnAspArgAspLeuGlu 81
Db 387 -----GGGACACCAATATTGTGTAC-----AAGAAATGACAGCAAGAC 425
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QY 82 ProIleAsnPhenArgLeuProGluAsnArgIleSerLysGluLysAspValLeuThrPhe 101
 DB 426 CCCATATCAGCGAC--CGGACCTCCAGGATTCATCAGAGAAATGAACATCTTGTTGTT 482
 QY 102 ArgProThrLeuLeuAsnAspThrGlyAsnIleThrCysMetLeuArgAsnThrThr 121
 DB 483 GTACCTCGCAAGGTGAGAGATCAGATATTTACTATTGTATGTAAGAACTCACTTAC 542
 QY 122 CysSerLeuValAlaPheProLeuGluValAlaGlnLysAspSer-----CysPheAsn 139
 DB 543 TECTCAAACTAAAGTAACCGTACTGTGTGAGAAATACCTCGCTGTGTGTACAGC 602
 QY 140 SerProMetLysLeuProValHisLysLeuValIleGluThrGlyIleGlnArgIleThr 159
 DB 603 AACACGGCCACCTTCCCA--CAGCGGCTCCACATTGCC--GGGATGGAAGCTCTGGG 656
 QY 160 CysProAsnValAspGlyIleThrPhe-----ProSerSerValLysProThrIleThrTrp 177
 DB 657 TCCCTTATGTG--AGTTATTTTAAAGATGAAATATATCATGTTACCCGAGGTCCAGTGG 713
 QY 178 TyrMetGlyCysTyrLysIleGlnAsnPhenAsnValIleProGluGlnMetLeuLeu 197
 DB 714 TATTAAGACTGT--AAACCTCTGCTTTGACACAGTGAGCTTTCCGAGTAAAGAT 770
 QY 198 SerPheLeuIleAlaLeuLeuSer-----AsnAsnGlyAsnIleThrCysValValThr 215
 DB 771 AAACGTCTGTGAGAAATGTGCTGAAGACACAGAGGGGACATATATGCTGATGTC 830
 QY 216 TyrProGluAsnGlyValArgThrPheHisLeuThrArgThrLeuThrValLysValIleGly 235
 DB 831 TATACCTTCCGGGGGAGAAATATCCGCTCACACAGTAAATCAATTTATCAACATAGAT 890
 QY 236 SerProLysAsnAlaValProValIleHisSerProAsnAspHisValValIleGlu 255
 DB 891 GAAACAAAGAGGAC--AGACCTGTATCTGAGCCCTCGAATAGACATC--GAA 944
 QY 256 LysGluProGlyGluGluLeuLeuLeuProCysThrValTyrPheSerPheLeuMetAsp 275
 DB 945 GGTGACCCAGGATCATGATGATACAACTGATCTGACGTCCAGGCCAGTTC----- 995
 QY 276 SerArgAsnGluValIleThrPheThrIleAspGlyLysLysProAspAspIleThrIleAsp 295
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 QY 296 ValThrIleAsnGluSer-----IleSerHisSerArgThr 307
 DB 1032 ATTTGAATGAAATGATTCATTTCTAGCTGAGACATCAATTTGTGAAACATCTTCAACC 1091
 QY 308 GluAspGlu---ThrArgThrGlnIleLeuSerIleLysLysValIleHisSerGluAspLeu 326
 DB 1092 AAAAGAAATATACACTCTCATTAACAACCTTACAGATTTCAAGATTAAGCCAGTTTAT 1151
 QY 327 LysArgSerTyrValCysHisAlaArgSerAlaLysGlyGluValAlaLysAlaLys 346
 DB 1152 CGCTATCCGTTATCTGTGTGTGTAAGACACA-----AATATTTTGTAGTGGGGCAT 1205
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 DB 1266 CTCACGGCTACAAATGTATGCTGTGTGATCATTAATGATTTCAAGGTGACATAGTG 1325
 QY 387 LeuPheTyrArgAlaHisPheGly-----ThrAspIleThrIleLeuAspGlyLysGlu 404
 DB 1326 CTTTGTACAGGAGACTCGCTCGTTTCTTCCTTCAAAAGCTCAAGTGAAGAGACA 1385
 QY 405 TyrAspIleTyrValSerTyrAlaArgAsnAlaGluGlu-----Glu 418
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 DB 1446 ACTTTGTGTTTAACTGTTCCTGAGCTCTGAGAGGACAGTTTGATTAACAAGCTGTTCC 1505
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 DB 1674 GAAGAAAT--AAATCTCTCTGCTGAGTTGAGAAATTCAGACTATATGAGAA 1727
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 QY 527 ---GluLysSerLysHisSerGlySerLysPheTrpLysAlaLeuArgLeuAlaLeu 544
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 QY 565 IleSerLeuAspHisValGlnArgArgSerArgLeuLysGluProProGluLeuGln 584
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 QY 605 LysSerSerAlaThrCysArgCysCysValIleThrTyrCysGluGluGluAsnHisLeuArg 624
 DB 1931 AGCAACACCTTATCACTGCGGTGACATGCAAAAGTGGGACAGGCCAA--GAACCTGCG 1987
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 QY 637 ---TrpGluThrHisLeuCysLysPro--ValProGlnGluSerGluThrGlnTrpIleG 655
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 QY 655 IAsnGlyThr 658
 DB 2099 AGAACAGGACT 2109

RESULT 13
 US-08-381-603-3
 ; Sequence 3, Application US/08381603
 ; Patent No. 5858355
 ; GENERAL INFORMATION:
 ; APPLICANT: Glorioso, Joseph C.
 ; APPLICANT: Evans, Christopher H.
 ; APPLICANT: Robbins, Paul D.
 ; TITLE OF INVENTION: Gene transfer for treating a connective tissue of a
 ; MAMMALIAN HOST
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Eckert Seamans Cherin & Mellott
 ; STREET: 1700 Market Street Suite 3232
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: USA

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      ZIP: 19103
      COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patentin Release #1.0, Version #1.25
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/381,603
      FILING DATE:
      CLASSIFICATION: 514
      ATTORNEY/AGENT INFORMATION:
      NAME: Gould, Jr., Lewis P.
      REGISTRATION NUMBER: 25,057
      REFERENCE/DOCKET NUMBER: 109070-11
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (215) 575-6000
      TELEFAX: (215) 575-6015
      TELEX: 866172
      INFORMATION FOR SEQ ID NO: 3:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 1782 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: double
      TOPOLOGY: linear
      MOLECULE TYPE: cDNA
      HYPOTHEICAL: NO
      ANTI-SENSE: NO
      IMMEDIATE SOURCE:
      LIBRARY: Mouse T-cell cDNA library
      CLONE: Mouse Interleukin-1 Receptor
      FEATURE:
      NAME/KEY: CDS
      LOCATION: 46..1776
      US-08-381-603-3

Alignment Scores:
  Pred. No.: 3,276-40      Length: 1782
  Score: 486.50           Matches: 153
  Percent Similarity: 46.04%      Conservative: 120
  Best Local Similarity: 25.80%    Mismatches: 225
  Query Match: 13.21%           Indels: 95
  DB: 2                      Gaps: 27

US-10-061-727-2 (1-687) x US-08-381-603-3 (1-1782)
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  166 ATGATATTGCGCAAGTGTCTTCTTACTCCAAATATAATGAC----- 207
  QY 62 HisSerIleGlyLeuThrLeuIleTrpTyrrTrpThrArgIleAspArgAspLeuGlu 81
  DB 208 -----GGCAGACACATATTTGGTAC-----AAGATGACAGCAAAACC 246
  QY 82 ProIleAsnPheArgLeuProGluAsnArgIleSerIysGluIysAspValLeuTrpPhe 101
  DB 247 CCCATATTCACCGGAC---CGGAGCTCCAGATCATCAGCAGAAATCAATCTTTGGTTT 303
  QY 102 ArgProThrIleuLeuAsnAspThrGlyAsnTrpThrCysMetLeuArgAsnThrThrTy 121
  DB 304 GATCTGCCAAGGTGAGAGACTCAGATATTAATTAATGATAGTAAGAACTCAACTTAC 363
  QY 122 CysSerIysValAlaPheProLeuGluValValGlnIysAspSer-----CysPheAsn 139
  DB 364 TGGCTCAAAACTAAAGTAACGTAACGTGTGTAGAGATGACCCGTGGCTGTGTATACAGC 423
  QY 140 SerProMetIysLeuProValHisIysLeuTyrrIleGluTyrrGlyIleGlnArgIleThr 159
  DB 424 ACACAGGCAACCTTCCCA---CAGCGGCTCCACATGTGC---GGGATGGAAGCTTGTG 477

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  QY 178 TyrMetGlyCysTyrrIysIleGlnAsnPheAsnValIleProGluGlyMetLeuAsn 197
  DB 535 TATTAAGAACTGT---AAACCTGTCTTTCAGCAACGTAGCTTCTTCGAGATTAAGAT 591
  QY 198 SerPheLeuIleAlaLeuIleSer-----AsnAsnGlyAsnTrpThrCysValValThr 215
  DB 592 AAACGTGTGTGAGGAATGTGCTGAAGAGCAGAGGGAGCATATATATGCTCATATGTC 651
  QY 216 TyrProGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValIysValValGly 235
  DB 652 TATAGCTCCGGGGAGAGCAATCCGGTCAACGAGTAAATCAATTATCACAATAGAT 711
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  DB 712 GAAACAGAGAGGAGC---AGACCTGTATCTGAGGCTCGGAAATGAGACGATC---GAA 765
  QY 256 LysGluProGlyGluGluLeuLeuIleProCysThrValTyrrPheSerPheLeuMetAsp 275
  DB 766 GCTGACCCAGATCAATGATGATCACTGATCTCAACGTACAGGCGCAGTTC----- 816
  QY 276 SerArgAsnGluValTrpTrpThrIleAspGlyIysLysProAspAspIleThrIleAsp 295
  DB 817 ---TCAGACCTGTCTACTCGAAGTGAATGATCA-----GAA 852
  QY 296 ValThrIleAsnGluSer-----IleSerHisSerArgThr 307
  DB 853 ATGAATGGAATGATGATTCATTTCTAGCTGAAGACTATCAATTTGTGGATATCTTCAACC 912
  QY 308 GluAspGlu---ThrArgThrGlnIleLeuSerIleIysValValThrSerGluAspLeu 326
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  QY 327 LysArgSerTyrrValCysHisAlaArgSerAlaIysGlyValAlaIysAlaIys 346
  DB 973 CGGTATCCGTATATCTGTGTGTGTAAAGACAC-----AARATTTTGAATCGGGCAT 1026
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  DB 1087 CTCACGGCTAACAAATGTAATGTGTGTGTGTCATCAATAAAGCTTCAAGGTGACATAGTG 1146
  QY 387 LeuPheTyrrArgAlaHisPheGly-----ThrAspGluThrIleLeuAspGlyIysGlu 404
  DB 1147 CTTTGGTACAGGACCTCGCTCGTCTTCTTCTTCAAAAGCTTCAATGAGTAAAGACA 1206
  QY 405 TyrAspIleTyrrValSerTyrrAlaArgAsnAlaGluGlu-----Glu 418
  DB 1207 TAGAGATGATATATTTCTTATCCCAAGACCTCGGAGAGGGCTCTTCTCAGACTTAGAT 1266
  QY 419 GluPheValLeuLeuThrIleuArgGlyValIleGluAsnGluPheGlyTyrrIysLeuCys 438
  DB 1267 ACTTTGTGTTTAAACGTGTGCTGAGCTTGGAGAGGACAGTTTGGATACAAAGCTGTC 1326
  QY 439 IlePheAspArgAspSerLeuProGlyGlyAsnThrValGluAlaValPheAspPheIle 458
  DB 1327 ATTTATGAGAGGATACATATGTTGAGAAAGATACATGAGGTTTACTAATAAGTAATGA 1386
  QY 459 GlnArgSerArgArgMetIleValValLeuSerProAsp----- 471
  DB 1387 AAGAAAGAGAGAGGCTGATTAATCATTTAGTGAAGATATGAGAGCTTCAAGCTGGCTG 1446
  QY 472 ---TyrrValThrGluIysSerIleSerMetLeuGluPheIysLeuGlyValMetCysGln 490
  DB 1447 GGCAGCTCATCTGAAGCAATAGCCATA-----TCAATGCTCATTCAG 1494
  QY 491 AsnSerIleAlaThrIysLeuIleValValGluTyrrArgProLeuGlu-----HisPro 508

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Db 1495 GAAAGATT-----AAATGCTCCTGCTGAGTTCAGAAATTCAGACTATGAGAA 1548
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 Db 1549 ATGCCAGATTCTATTCACTTCCTTAAGAGAAACAGAGATTCATTGCTGGTCAGAGAAC 1608
 Oy 527 -----GluYserSerHisSerGlySerIySerPheTrrpYsAlaLeuArgLeuAlaLeu 544
 Db 1609 TTTCAAGAAAGACCACTGCTCAAGAACAGAGCTTCTGAAAACTTAAGATACAGATG 1668
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 Oy 565 IleSerLeuAspHisValGlnArgArgArgSerArgLeu 577
 Db 1708 CTAACTCTGATCTCTGCGGACACTTAAGAGAAACTG 1746

US-08-924-376-3
 Sequence 3, Application US/08924376
 Patent No. 6159464
 GENERAL INFORMATION:
 APPLICANT: Glorioso, Joseph C.
 APPLICANT: Evans, Christopher H.
 APPLICANT: Robbins, Paul D.
 APPLICANT: Bandara, Geethani
 TITLE OF INVENTION: Gene Transfer For Treating a
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Eckert Seamans Cherin & Mellott
 STREET: 1700 Market Street Suite 3232
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/924,376
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/027,750
 FILING DATE: 08-MAR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Gould, Jr., Lewis F.
 REGISTRATION NUMBER: 25,057
 REFERENCE/DOCKET NUMBER: 109070-3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 575-6000
 TELEFAX: (215) 575-6015
 TELEX: 866172
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1782 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 IMMEDIATE SOURCE:
 LIBRARY: Mouse T-cell cDNA Library
 CLONE: Mouse Interleukin-1 Receptor
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 46..1776

US-08-924-376-3
 Alignment Scores:
 Pred. No.: 3,276-40 Length: 1782
 Score: 484.50 Matches: 153
 Percent Similarity: 46.04% Conservative: 120
 Best Local Similarity: 25.80% Mismatches: 225
 Query Match: 13.21% Indels: 95
 DB: 3 Gaps: 27
 US-10-061-727-2 (1-687) x US-08-924-376-3 (1-1782)
 Oy 34 GlnIleGlnValPheGluAspGluProAlaArgIle----- 45
 Db 106 GAGATTGACGTATGATACAGAAATATCCAAATCAGATCGTTTGTATTATCTGTAATGAA 165
 Oy 46 -----LysCyProLeuPheGluHisPheLeuYsPheAsnYrSerThrAla 61
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 Oy 62 HisSerAlaGlyLeuThrPheLeuIleTrrpYrThrArgGlnAspArgLeuGlu 81
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 Qy 367 ThrValLeuLeuValValIleuIleuValValTyrHisValTyrTrpLeuGluMetVal 386
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 Qy 405 TyrAspIleuTyrValSerTyrAlaArgAsnAlaGluGlu-----Glu 418
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 Qy 472 ---TyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyValMetCysGln 490
 Db 1447 GGCAGTATCTGAAGAGCAATATAGCCATTA-----TACATCTCTATCCAG 1494
 Qy 491 AsnSerIleAlaThrLysLeuIleValValGluTyrArgProLeuGlu-----HisPro 508
 Db 1495 GAAGATTT-----AAATCGTCTGCTTGTAGTGAAGAAATCCAAAGACTATGAGAA 1548
 Qy 509 HisProGlyTyrLeuGln---LeuLysGluSerValSerPheValSerTrpLysGly--- 526
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 Qy 527 -----GluLysSerLysHisSerLysSerLysPheTrpValAlaLeuArgLeuAlaLeu 544
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 Qy 545 ProLeuArgSerLeuSerAlaSerSerGlyTyrAsnGluSerCysSerSerGlnSerAsp 564
 Db 1669 CCAAGCCCAAGGAGATCA-----CCATGTCTTAACACCGCTTA 1707
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Search completed: April 30, 2003, 13:03:13
 Job time : 93 secs

GenCore version 5.1.4 p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 30, 2003, 11:50:55 : Search time 152 Seconds

(without alignments)
5340.616 Million cell updates/sec

Title: US-10-061-727-2

Perfect score: 3669

Sequence: 1

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Delop 6.0 , Delext 7.0

Searched: 746064 segs, 590810554 residues

Total number of hits satisfying chosen parameters: 1492128

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cg2n_1/USPTO.spool/US10061727/runat_23042003_083118_8008/app_query.fasta_1.839

-DB=Published Applications NA -OFMT=fastcap -SUFFIX=rnpb -MINMATCH=0.1

-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -SPART=1 -END=1 -MATRIX=10sums62

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-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTPMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0

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Database :

Published Applications NA:

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14: /cg2n_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	DB ID	Description
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2	1934	52.7	1077	9 US-10-215-211-5
3	1930	52.6	2733	9 US-09-935-868-27
4	825	22.5	2061	9 US-10-011-548-3

5	800	21.8	1737	9 US-10-011-548-1	Sequence 1, Appli
6	767	20.9	2537	9 US-10-011-548-34	Sequence 34, Appli
7	531	14.5	287	10 US-09-864-761-32830	Sequence 32830, A
8	528	14.4	1626	10 US-09-981-421-3	Sequence 3, Appli
9	528	14.4	1626	12 US-10-157-447-1	Sequence 1, Appli
10	495	13.5	2314	9 US-10-011-548-9	Sequence 9, Appli
11	495	13.5	2681	9 US-10-212-287-6	Sequence 6, Appli
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15	482	13.1	4989	10 US-09-899-980A-3	Sequence 3, Appli
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19	463.5	12.6	2058	10 US-09-899-980A-4	Sequence 14, Appli
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21	446.5	12.2	1845	9 US-10-212-287-1	Sequence 15, Appli
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31	314	8.6	1366	9 US-10-199-209-12	Sequence 358, App
32	259	7.1	616	9 US-09-764-868-358	Sequence 1, Appli
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ALIGNMENTS

RESULT 1
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; Sequence 3, Application US/10215211
; Publication No. US20030049255A1
GENERAL INFORMATION:
APPLICANT: Sims, John E.
TITLE OF INVENTION: INTERLEUKIN-1 RECEPTORS IN THE TREATMENT OF DISEASES
FILE REFERENCE: 3321-A
CURRENT APPLICATION NUMBER: US/10/215,211
PRIOR FILING DATE: 2002-08-07
PRIOR APPLICATION NUMBER: US 60/310,789
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 1713
TYPE: DNA
ORGANISM: Homo sapiens
NAME/KEY: CDS
LOCATION: (1) (1713)
OTHER INFORMATION:
US-10-215-211-3
Alignment Scores:
Pred. No.: 5.71e-290
Score: 2580.00
Length: 1713
Matches: 487

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RESULT 4
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Sequence 3, Application US/10011548
Publication No. US20030055218A1
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
Debets, Johannes Eduard Maria
Antonius
Sana, Theodore R.
Bazan, J. Fernando
Kastelen, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,548
FILING DATE: 22-Oct-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/173,151
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-9196
TELEFAX: (650) 496-1200
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2058
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-011-548-3

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US-10-061-727-2 (1-687) x US-10-011-548-3 (1-2061)
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OY 621 AsnHisLeuArgAsn-----LysSerArgAlaGluIleHis 632
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RESULT 5
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; Sequence 1, Application US/10011548
; Publication No. US2003005218A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; Debets, Johannes Eduard Maria
; Antonius
; Sana, Theodore R.
; Bazan, J. Fernando
; Kastelein, Robert A.
; TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and
; Methods
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESS: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/011,548
; FILING DATE: 22-Oct-2001
; CLASSIFICATION: <Unknown>

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/173,151
FILING DATE: <unknown>
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1737 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: cDNA
HYPOTHETICAL: YES
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LOCATION: 1..1737
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Percent Similarity: 51.44% Conservative: 96
Best Local Similarity: 35.14% Mismatches: 208
Query Match: 21.80% Indels: 78
DB: 9 Gaps: 24
US-10-061-727-2 (1-687) x US-10-011-548-1 (1-1737)

Qy 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAsp--- 19
Db 7 CTGCACTAATTA-----GTGTCAACAATGCTCACTGATCTTACTCTTCTGATTTT 60
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Db 61 CTTTCACTGATGCTGCTCATTTGATGCTGATGAT---CTCAAGACATACATGAGCTTTG 117
Qy 39 GluAspGluProAlaArgGlyIleCysProLeuPheGluIlePheLeuLysPheAsnTyr 58
Db 118 GCAAGTAAACAGCCAGCAAGTAATGTCCTTTTCAAGTTATATTCATCCACCACTAT 177
Qy 59 SerThrAlaHisSerAlaGlyLeuThrLeuIleThrTyrTrpThrArgGlnAspArgAsp 78
Db 178 AGCAGGCGCCAGAGCACTGGAGCTTATATGTGTAC-----AAAACAAGGTGAT 231
Qy 79 LeuGluGluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspVal 98
Db 232 TTGAAAGAGCCCATCATCTT-----TCAGAGTCAAGATGACCAAGAGATTTCA 285
Qy 99 LeuTyrPheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsn 118
Db 286 ATATGTTTCACTCAGCTGAGGCACAAGACAGTGAATTTCACTTGTGTTTAAGAAC 345
Qy 119 ThrThrTyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSer----- 136
Db 346 TCACATATTTGATGATGAGTGAATGATGCTTGTGATGATGATGATGATGATGATGATG 405
Qy 137 CysPheAsnSerProMetLysLeuProValHisLysLeuTyrIleGluTyrGly----- 154
Db 406 TGCTACAAACAGCAGATCCCG-----TTTATGAAAAATCTGAATC 447
Qy 155 -----IleGlnArgIleThrCysProAsnValAspGlyTyrPheProSerSerValLys 172
Db 448 ACTAAAGAAGAAGATCTCTGATCCAGACATGATGATTAATAAGTCAGATCAGAG 507
Qy 173 ProThrIleThrTyrTyrMetGlyCysTyrLysIleGlnAsnPheAsnValIlePro 192
Db 508 CTTGATGTTGTGTGTATTAAGATGACCAAAATGTGAGAGCAATATATATGACAG 567
Qy 193 GluGlyMetAsnLeuSerPheLeuIleAlaLeuIleSerAsnGlnLysAsnTyrThrCys 212
Db 568 AAAGAAATGCTCTTCTGATCCAAAGATTCAGAAAGATGAGAAATTTACATGT 627
Qy 213 ValValThrTyrProGluAsnGlyArgThrPheHisLeuThrArgThrValLys 232
Db 628 GAACCTTAATAT-----GAAGAAACTT-----GTAAGACGACAACTGAATGAAA 675
Qy 233 ValValGlySerProLysAsnAlaValPro---ProValIleHisSerProAsnAspHis 251
Db 676 GTTACAGCTTACTACACAGCAAGCTCCAGCATGTGCTCCCATGAGAAATCAAGCA 735
Qy 252 ValValTyrGluLysGluProGlyGluGluLeuLeuIleProCysThrValTyrPheSer 271
Db 736 AGTGTATATATGTCAGCTGGGAGAACCTCTGAACATCCCTGCAAGCATTTCTTGA 795
Qy 272 PheLeuMetAspSerArgAsnGluValTyrTrpThrIleAspGlyLysProAspAsp 291
Db 796 TTCACTGAGAGCTGGGCAATGATCTACG---ATGAAGAGAGAAAG----- 843
Qy 292 IleThrIleAspValThrIleAsnGluSerIleSerHisSerArgThrGluAspGluThr 311
Db 844 -----TTTATTTGAAGACTGCGCAGGTCACTTAAG---GAAGGTGAATA 885
Qy 312 Arg-----ThrGlnIleLeuSerIleLysLys 320
Db 886 AGGCTTCTCAAGACATCTTGAGAAAGAAAGACTTCAATTTGGACATCATCTTGAATCA 945
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db 946 GTTGTGAAAGCTGACCTG---GCCAATTATATCCGTCATGTGTAAGAAACGAAATGAGCG 1002

QY 142 MetLysleuProValHisLysLeuTyrIleGluTyrGly-----IleGlnArg 157
DB 358 ATGAAG-----TATTTGAAAAGAGCTGAACCTTAGCAAAACCAAGAA 399
QY 158 ILeuTyrProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrp 177
DB 400 ATTTCATGCGGTGACATGAGATATTTTCTACGCCAACCAAGAACCTGAATCCCTTGG 459
QY 178 TyrMetGlyCysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeu 197
DB 460 TACAAGAAATGAGAGCAAAAACATGAGAGCCAGATATGTTTCAAAAGAGATCTCTG 519
QY 198 SerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValAlaThrTyrPro 217
DB 520 CTTAATAAGAGAGTCAGAGAGATGACATGTGAATTTATACCTGTGAATTAATAAT 576
QY 218 GluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysValAlaGlySerPro 237
DB 577 ---GAGAGCTTTTGTGAGAGAACTACTGAATTAAGCTTTACA-----GCCCT 624
QY 238 LysAsnAlaValProProValIleHisSerProAsnAspHis-----ValValTyrGlu 255
DB 625 CTGACTGATAGCCACCAAGCTTTTGTATCTATGAAAAGTAACTGACAAATTCAGAG 684
QY 256 LysGluProGlyGluGluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAsp 275
DB 685 ACCAGCTGGGTGACTGCTAATCTACCTGACAGAGCTTTCTTGGGTACAGCGAGAT 744
QY 276 SerArgAsnGluValTrpTrpThrIleAspGlyLysProAspAspIle----- 292
DB 745 GTCACTCTTTAATTTACTGATGAAAGAGAAATTAATTAAGATCTGATGAAT 804
QY 293 -----ThrIleAspValThrIleAsnGluSerIleSerHisSerArgThrGluAsp 309
DB 805 CGAGTTGGGAAAGTGCATTAAGAAAT-----CTTAAGAGCATCTGGGAGAACAG 855
QY 310 GluThrArgThrGlnIleLeuSerIleLysLysValThrSerGluAspLeuLysArgSer 329
DB 856 GAAGTTTCATCTCATTAAT--GTGAGCTGTGGAAGAGGACTTG---GGAAT 909
QY 330 TyrValCysHisAlaArgSerAlaLysGlyGluValAlaLysAlaValLysGln 349
DB 910 TACTCTGTTATGTTGAAATGGAATGAGAGCT-----CGACAGCCAGGCTTCTCT 963
QY 350 LysValProAlaProArgTyrThrValGluLeuAlaCysGlyPheGlyAlaThrValLeu 369
DB 964 CATTAACGAGAGCTAATGTACACAGTGAACTTGCTGAGGCTTGTGCTATACTCTTG 1023
QY 370 LeuValValIleLeuIleValValTyrHisValTyrTrpLeuGluMetValLeuPheTyr 389
DB 1024 CTGCTTGATGTTGGTGGACATCTACAGGTGTAAGAAATGAAATCATCTCTTCTAC 1083
QY 390 ArgAlaHisPheGlyThrAspGluThrIleLeuAspGlyLysGluTyrAspIleTyrVal 409
DB 1084 AGGATCATTTTGTAGCTGAAGCTCGATGAGACAAATTAAGATTTGATGACTACTTA 1143
QY 410 SerTyrAlaArg-----AsnAlaGluGluGluGluPhe 420
DB 1144 TCATACCAAAATGATCTCTGACAGTGAAATCAAGAGCTGGGAGAAAGAGCTTTT 1203
QY 421 ValLeuLeuThrLeuArgGlyValLeuGluAsnGluPheGlyTyrLysLysCysIlePhe 440
DB 1204 GCCCTTGAATCTTACTGATATGTTGAAGACATTAATGATTAAGTTGTTATACCA 1263
QY 441 AspArgAspSerLeuProGlyLysAsnThrValGluAlaValPheAspPheIleGlnArg 460
DB 1264 GATAGAGATTTAATCCCACTGACATCAATGAAGATGTGCAAGATGTGATGATCA 1323
QY 461 SerArgArgMetIleValValLeuSerProAspTyrValThrGluLysSerIleSerMet 480
DB 1324 AGCAAGCGGCTATATATGTCTACGACCCCAATTAAGTGAAGGCGGCTGAGACATC 1383

QY 481 LeuGluPheLysLeuGlyValMetCysGlnAsnSerIleAlaThr-----LysLeu 497
DB 1384 -----TTGACTGGAACCAAGACTTGCAAATATGCTTGTGATGAGAAATTAAGTG 1437
QY 498 ILeuValAlaGluTyrArgProLeuGluHisProHisProGlyIleLeuGlnLeuLysGlu 517
DB 1438 ATTCTAATTAATGATGAGGAACTGAGA-----GGAATTTATGAACTACCAAGAG 1485
QY 518 -----SerValSerPheValSerTyrPheGlyGluLys 528
DB 1486 GTGAGGCCCTGAGACACCACTCAAGCTCTGACGGTCATTAATATGATGACCAAAA 1545
QY 529 SerLysHisSerGlySerLysPheThrPylsAlaLeuAlaGlyLeuAlaLeuProLeuArg 547
DB 1546 TGCAACAAGTTGAACCTCAAGTTCTGAAACGTTTAACAGTGAATATGCTTTTAAGAG 1605
QY 548 -----Ser 548
DB 1606 ATAGAACCCATTACATGACAGAGCTTTAGATGTCACTGAGCAAGGCTTTGGGAG 1665
QY 549 LeuSerAlaSerSerGlyTyrAsnGluSerCysSerSerGlnSerAspIleSerLeuAsp 568
DB 1666 CTGACAGACTGTCTGGCCATTTCCATGCGCGGACCTCCACAGCTCTAGCCACTGCC 1725
QY 569 HisValGlnArg-----ArgSerArgLeuLysGluProPro 581
DB 1726 CATCAAGATCTCGTTTCTACCTTTCACAAACGTAACATTCACAAATGCGTCAGAAAC 1785
QY 582 GluLeuGlnSerSerGluArgAlaAlaGlySerProProAlaProGly**MetSerLys 601
DB 1786 TACTACCGAAGCTATGATGACAGCTA-----CTCTTACCGGACCTGCTCTTACC 1839
QY 602 HisArgGlyLysSerSerAlaThrCysArgCysCysValThrTyrCysGluGlyLys 621
DB 1840 TCCATAGGCAATCAGCATACTACTGTAACTCCCTATGACATCATCAAGGGCAGCGG 1899
QY 621 HisLeuArgAsnLysSerArgAlaGluIleHisAsnGlnProGlnTrpGluThrHisLe 641
DB 1900 CCACAGCAAAATGACACAGAGACAGAAATCCAGATAGGCCCCACAAACAGTGCATC 1959
QY 641 uCysLysProValProGlnIle-----SerGluThrGlnTrpIleGln 655
DB 1960 CTGCGCGTG--TTGCCAAGGAGACAGATATATCAAGTGAATATGTGACAG 2010
RESULT 7
US-09-864-761-32830
Sequence 32830, Application US/09864761
Patent No. US2002048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aomic-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
SEQ ID NO 32830
LENGTH: 287
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC008249.14
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
OTHER INFORMATION: EST HUMAN HIT: BR89231.1, EVALU0.00e+00
OTHER INFORMATION: NT HIT: APL6736.1, EVALU0.00e+00
OTHER INFORMATION: SWISSPROT HIT: Q02955, EVALU0.00e-03
US-09-864-761-32830

Alignment Scores:
Pred. No.: 1,11e-52 Length: 287
Score: 531.00 Matches: 95
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 14.47% Indels: 0
Gaps: 0
DB: 10

US-10-061-727-2 (1-687) x US-09-864-761-32830 (1-287)

23 ArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAspGluPro 42
3 CGCTGGCATGATGAGGAGCTAGACACCATGAGGCAATCCAGTGTGGAAGATGAGCCA 62
43 AlAaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThrAlaHis 62
63 GCTGCGATCAAGTGCACCTCTTGAACACTTCTTGAATTCACCTACAGCAGCCCAT 122
63 SerAlaGlyLeuThrLeuIleTyrTyrThrArgGlnAspAspLeuGluGluPro 82
123 TCGACTGACCTACTCTGATCTGGATTTGACAGCGAGGACCGGACCTTGAGAGCCA 182
83 IleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTyrPheArg 102
183 ATTAACTTCGCCCTCCCGAGAGACCGCATTTAGTAAGAGAAAGATGCTGTGCTCGG 242
103 ProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArg 117
243 CCCACTCTCCCTCAATGACATGCGCAACTATATCTGCAATGTTAAGG 287

RESULT 8
US-09-981-421-3
Sequence 3, Application US/09981421
Patent No. US20020098185A1
GENERAL INFORMATION:
APPLICANT: Sims, John E.
APPLICANT: Mohler, Kendall M.

APPLICANT: Born, Teresa L.
TITLE OF INVENTION: METHODS FOR TREATING IL-18 MEDIATED DISORDERS
FILE REFERENCE: 3086-A
CURRENT APPLICATION NUMBER: US/09/981,421
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: US 60/241,408
PRIOR FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 1626
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1) ..(1626)
OTHER INFORMATION:
US-09-981-421-3

Alignment Scores:
Pred. No.: 4.76e-51 Length: 1626
Score: 528.00 Matches: 174
Percent Similarity: 46.03% Conservative: 93
Best Local Similarity: 30.00% Mismatches: 215
Query Match: 14.39% Indels: 98
Gaps: 27
DB: 10

US-10-061-727-2 (1-687) x US-09-981-421-3 (1-1626)

4 LeuTyrCysValIleSerLeuTyrPheTyrGlyIleLeuGlnSerAspAlaSerGluArg 23
28 CTTTGCGTCTTATATCTCTA-----AGCACTGCAAGATCT 63
24 CysAspAspTrpGlyLeuAspThrMetArg---GlnIleGlnValPheGluAspGluPro 42
64 TGT-----ACTTCAGCTCCCGACACTTACTGTGTGTAAGGGAACCT 105
43 AlAaArgIleLys---CysProLeuPheGluHisPheLeuLysPheAsnTyrSerThrAla 61
106 TTCTATCTGAACCATTCG-----TCGTTTCATCTTGA 138
62 HisSerAlaGlyLeuThrLeu---IleTyrTyrThrArgGlnAspAspLeuGlu 80
139 CATGAGATTGAAACACACCAAGCTGTGACAAAGAGTGATCAGACAGAACTGTC 198
81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTyr 100
199 GAG---CTGAACCCAGG---ACTTCCTGAGATGCTTTCATGATCTGTGTTGAG 252
101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThr 120
253 TTTTGCCAGCTTACGTTGATGACACAGGATCTTATCTTTTCCAAATGAAATTAATTA 312
121 TyrCysSerLysValAlaPheProLeuGluValGln-----LysAspSerCysPhe 138
313 CAG-----AAATGAAATTAATTAATGATCAGAAAGAAATTAACACACTGTTTC 360
139 Asn-----SerProMetLysLeuProValHisLysLeuTyrIleGluTyrGly 154
361 ACTGAAGACAGACTACTGTAATAATTTGGAAGTTAATAAATTTT-----408
155 IleGlnArgIleThrCysProLeuAsnValAspGlyTyrPheProSerSerValLysProThr 174
409 ---CAGTTACCTGTGAAGC-----AGTTACATCAAAACAGCTGCAACAGACA 456
175 IleThrTyrIleTyrMetGlyCysTyrLysIleGlnAsnPheAsnValIleProGlu--- 193
457 ---TCATGTATAGAAGACTTAATAAAGCTACTGAGAGAAATTAATAAACCAGACATA 513
194 GlyMetAsnLeuSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysVal 213
514 AAGAAAGACCGCAGATT-----GAGATCAGGGGTATTAATCTCTGCGTG 558


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QY 214 ValThrTyrProGluAsnGluValGlyThrPheHisLeuThrArgThrLeuThrValIleVal 233
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QY 234 ValGlySerProIleAsnAlaValProProValIleHisSerProAsnAspHisValVal 253
DB 619 GTGGAAGATCGCATTAATTAATGATCGGTTCTTGTGACCAAAAGCTTAACATGTGCA 678
QY 254 TyrGluValGluProGluIleuLeuIleProCysThrValTyrPheSerPheLeu 273
DB 679 GTGGAATTA-----GAAAAAAGCTAAGGCTCAACTGC-----TCTCTTGG 720
QY 274 MetLeuSerArgAsnGluValTyrThrIleAspGlyValProAspAspIleThr 293
DB 721 CTGAATGAAGAGATTAATTAATGATTTGGGGAAGAAATGATCGGATCTCTAT 780
QY 294 IleAspValThrIleAsnGluSerIleSerHisSerArgThrGluAspGluThrArgThr 313
DB 781 ATA-----CATGAAGAGAAAGAAATGAAATGAAATTAATTAATGACT 813
QY 314 -----GlnIleLeuSerIleValIleValIleValIleValIleValIleValIleVal 325
DB 814 CCAGAGGCAATGCGATCGTCAAAAGATTAATGAAATTAATTAATGAAAGCAAT 873
QY 326 LeuLysArgSerTyrValCysHisAlaArgSerAlaValGlyGluValAlaIleValAla 345
DB 874 CTAATGTTTAATTAATTAATTAATGACATGCGCAGCAAGGAGGACAGACCAAAAGCTTC 933
QY 346 LysValIleGluVal-----ValProAlaProArgTyrThrValGluLeu 360
DB 934 ATCTTGAGAGAAAGACAGACATGCTGATATCCAGGCCAGCTTCACA----- 984
QY 361 AlaCysGlyPheGlyAlaThrValLeu-----ValValIleLeuIleValVal 377
DB 985 ---AGAGAGATGATCATACGCTTTTATCTTGTGCGCAGAGTGTGCTAATGATCTGTG 1041
QY 378 TyrHisValTyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGlu 397
DB 1042 TGTGTCAATTAATGAAGTGAATGCTGTTCTAATTAATGAATTAAGAGAGAGATGAA 1101
QY 398 ThrIleLeuAspGlyValGluTyrAspIleTyrValSerTyrAlaArg----- 413
DB 1102 ACATTAACAGATGAGAAACATATGATGCTTGTGTCTTAACCTAAAGAAATGCCGACT 1161
QY 414 ---AsnAlaGluGluGluValPheValLeuThrLeuArgValValLeuGluAsnGlu 432
DB 1162 GAAATGAGAGAGACACACTTTCCTGTGAGATTTTGCCAGGAGTGTGAGAGAAACAT 1221
QY 433 PheGlyTyrIleLeuCysIlePheAspArgAspSerLeuProGlyIleAsnThrValGlu 452
DB 1222 TTGGGTAATTAATGATCATATTTGAAGGAGTGTAGCTGAGAGAGCTGTGTTGAT 1281
QY 453 AlaValPheAspPheIleGluArgSerArgArgMetIleValValLeuSerProAspTyr 472
DB 1282 GAAATCACTACCTAGTAGAGAAAGCCGAAAGCTAATCATTCCTAATTAAGTAAGTTAT 1341
QY 473 ValThrGluValSerIleSerMetLeuGluPheLysLeu-----GlyValMetCysGlnAsn 491
DB 1342 ATGCTTAATGAGTCAAGTATGAACTTGAAGAGAGCTCAATGAAGCATTTGAGAAAGA 1401
QY 492 SerIleAlaThrIleLeuIleValValGluTyrArgProLeuGluHisProHis----- 509
DB 1402 AAAAAT-----AAAAATATCTTAATTAATGAATTAACCTGTACTGACTTCAATCTTG 1455
QY 510 ProGlyIleLeuGluIleuValGluSerValSerPheValSerTyrPlyGlyGlyValSer 529
DB 1456 CCGCAATCACTAAGCTTTGAATATCAACAGATTCGAAAGGAGGAGCCGATTAATCT 1515
QY 530 LysHisSerGlySerIlePheTyrPlyValAlaLeuArgLeuAlaLeuArgSerLeu 549
DB 1516 CTTTCTTAATCAAGGTTCTGAGAAAGACTTCTTAATTAATGCTCAACAAACAGTC 1575

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US-10-157-447-1
Sequence 1, Application US/10157447
Patent No. US20020143155A1
GENERAL INFORMATION:
APPLICANT: Parnet, Patricia et al.
TITLE OF INVENTION: Receptor Designated ZPI
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/157,447
FILING DATE: 28-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/578,178
FILING DATE: <Unknown>
APPLICATION NUMBER: 09/110,618
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2619
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1626 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: hu2F1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1626
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 58..1623
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1..57
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-157-447-1
Alignment Scores:
Pred. No.: 4.76e-51
Score: 528.00 Length: 1626
Percent Similarity: 46.03% Matches: 174
Best Local Similarity: 30.00% Conservative: 93
Query Match: 14.39% Mismatches: 215
DB: 12 Gaps: 98
US-10-061-727-2 (1-687) x US-10-157-447-1 (1-1626)
QY 4 LeuTyrCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAlaSerGluArg 23
DB 28 CTTGGGCTTATATCTGTA-----AGCACTGCAAGAACTCT 63

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Oy	24	CysaspasprtrpglyLeuasprthmetArg---	GlnileglValPhegluspgluPro	42
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Oy	43	AlaArgileLys---	CysProleuPheGluWhiSphleuLysPheasnTrSerThra	61
Db	106	TTCTATCTGAAACATTGC-----	TCGtGTTCACTGTGA	138
Oy	62	HisserAlaGlyLeuthrLeu---	IleTrpTyrrTrpThrArgGlnAspArgSpleuGlu	80
Db	139	CATGAGATTGAAACACACACCAAAAGCTGGTACAAAAGCAGTGAATCAcAGAACATGTG		198
Oy	81	GluProIleasnPheAsnArgleuProGluAsnArgIleSerTrsGluLysAspValleuTrp		100
Db	199	GAG---CTGAACCCAAAG--AGTTCCTCAGAAATTCCTTGACATGTTGTGTGGAG		252
Oy	101	PheArgProthrIleLeuLeuAsnAspThrGlyAsnTrpTrpCysMetLeuArgAsnThrTrh		120
Db	253	TTTGGCCAGTTGAGTTGAATGACACAGCACTTACTTTTCCAAATGAAAATTATACT		312
Oy	121	TyrCysSerLysValAlaPheProleuGluValAlaGln-----LysAspSerCysPhe		138
Db	313	CAG-----AAATGAATTAATGTCATCAGAGAATAAACAACAGCTGTTC		360
Oy	139	Asn-----SerProMetLysLeuProValHisLysLeuTyrIleGluTyrGly		154
Db	361	ACTGAAGAACAAGTAACTAAATTTGTGGAAATTTAAAAATTTTTT-----		408
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Oy	175	IleThrTrpTyrMetGlyCysTrpLysIleGlnAsnPheAsnAsnValIleProGlu---		193
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Oy	194	GlyMetAsnLeuSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrTrpCysVal		213
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Oy	214	ValThrTyrProGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysVal		233
Db	559	CATTTCCTTCATCATTAAGAAACATATTATTAATCAcCAAAACCTTCATATTAACATA		618
Oy	234	ValGlySerProLysAsnAlaValProProValIleHisSerProAsnAspHisVal		253
Db	619	GTGGAAGATCGCAGTAATATAGTTCGGTCTTCTGGACCAAAAGCTTAACATGTTGCA		678
Oy	254	TyrGluLysGluProGlyGluGluLeuLeuIleProCysThrValTyrPheSerPheLeu		273
Db	679	GTGCAATTA-----GGAAGAAACCTTAAGCCTCAACTGC-----TCGGCTTG		720
Oy	274	MetAspSerArgAsnGluValTrpThrIleAspGlyLysLysProAspAspIleThr		293
Db	721	CTGAATGAAGACAGTAAATTATTTATGATGTTTGGGACGAAGAAATGCATGCATCTAAT		780
Oy	294	IleAspValThrIleAsnGluSerIleSerHisSerArgThrGluAspGluThrArgThr		313
Db	781	ATTA-----CATGAAGAGAAAGAAATGAGATTAATGACT		813
Oy	314	-----GlnIleLeuSerIleLysLysValThrSerGluAsp		325
Db	814	CCAGAAAGCAAAATGCATCTCTTCAAAAGTATGAGAAATGAAAATTTATGTCGAAGCAAT		873
Oy	326	IleuLysArgSerTrpValCysHisIleAlaArgSerAlaLysGlyGluValAlaLysAla		345
Db	874	CTAAATGTTTAAATATATATTCACGTGTGGCCAGACGGAGGACACACCAAAAGCTTC		933
Oy	346	LysValLysGlnLys-----ValProAlaProArgTyrTrpThrValGluLeu		366
Db	934	ATCTTGCTGAGAAAGACACATGCTGATATCCAGGCAcGtCTTCAC-----		984
Oy	361	AlaCysGlyPheGlyAlaThrValLeuLeu-----ValValIleLeuIleValVal		377

FILING DATE: 17-NOV-1997
 APPLICATION NUMBER: US 60/078,008
 FILING DATE: 12-MAR-1998
 APPLICATION NUMBER: US 60/081,883
 FILING DATE: 15-APR-1998
 APPLICATION NUMBER: US 60/095,987
 FILING DATE: 10-AUG-1998
 APPLICATION NUMBER: US 60/078,416
 FILING DATE: 18-MAR-1998
 APPLICATION NUMBER: US 60/062,066
 FILING DATE: 15-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Ching, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DX0767X
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650)852-9196
 TELEFAX: (650)496-1200
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2314 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 109..1905
 SEQUENCE DESCRIPTION: SEQ ID NO: 9:
 US-10-011-548-9

Alignment Scores:
 Pred. No.: 6.05e-47 Length: 2314
 Score: 495.00 Matches: 181
 Percent Similarity: 44.25% Conservative: 127
 Best Local Similarity: 26.01% Mismatches: 288
 Query Match: 13.49% Indels: 104
 Gaps: 27

US-10-061-727-2 (1-687) x US-10-011-548-9 (1-2314)

QY 11 TyrPheTyrGlyIleLeuGlnSerAspAlaSerGluArgCysAspAspTyrGlyLeuAsp 30
 DB 128 TATTCTTGGCTTGGTGGAGCA-GAGCAATTAAGGATTAATATTCTGTTGTTCC 186
 QY 31 ThrMetArgGlnIleGlnValIlePhe-----GluAspGluProAlaArgIleLeuGln 47
 DB 187 ACAAAAAACCTCTTGGACATATTCTCAAGAGTGAAGAGAAATTTGCTTATTTTGT 246
 QY 48 ProLeuPheGlu-----HisPhe----- 53
 DB 247 GATTACACGAGCCACAGAAATCAATTTCTGCCACAGAAATGCACTCTACCAAAACAA 306
 QY 54 -----LeuLysPheAsnTyrSerThrAlaHisSerAlaGlyLeuThrLeuIle 69
 DB 307 GTCCCTGAGACCTCGCCCTTCATGGTAAAGCAACCTATCT-----GATGTCGA 357
 QY 70 TyrTyrTyrThrArgGlnAspArgAspLeuGluProIleAsnPheArgLeuProGlu 89
 DB 358 TGGTACCAACAACCTTGGAATGAGATCCATTAGAGACATTAAGAAAACCTATCTCT--- 414
 QY 90 AsnArgIleSerLysGlnLysAspValLeuTyrPheArgProThrLeuLeuAsnAspThr 109
 DB 415 ---CACATCAATCAAGACAATGATGACCTTCACTTTTGAACCCAGGGGTGAATATCT 471
 QY 110 GlyAsnTyrThrCys-----MetLeuArg-----AsnThrThrTyrCysSer 123
 DB 472 GGGTCATATATTGTGAGACCAAGATGATTAAGAGCCCTTATGATGAGCTGTGTGTC 531
 QY 124 LysValAlaPheProLeuGlnValAlaGlnLysAspSerCysPheAsnSerProMetLys 143
 DB 532 AGATGATTTTAAAGTTAAGCCCAAGACAATGATCTCTGTGATGATTCGACATCA--- 588

QY 144 LeuProValHisLysLeuTyrIleGluTyrGly---IleGlnArgIleThrCysProAsn 162
 DB 589 -----CATAGCAAGACCTACTCTTGGAGACATGCGCTCATATTTCTGCCCCAGT 639
 QY 163 ValAspGlyTyrPheProSerSerValLysProThrIleThrTyrPheTetGly----- 180
 DB 640 CTCACGTGCGCA---AGTATGACACAAAGTCCAGGGGTACCTGTGACAAAGATGAAAA 696
 QY 181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
 DB 697 CTCCTCTGTGGAAGAAGACCAAGATCGATGATGATGATGATGATGATGATGATGAT 741
 QY 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
 DB 742 -----TATGACTATCACCAGGACCAATGATGATGATGATGATGATGATGATGAT 795
 QY 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValAlaGlySerProLysAsnAla 240
 DB 796 AGTCTGTGACAGTCAGACGCTGTGTTCAAGTGAACCACTTGGAGACACTAACTC 855
 QY 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGluGlu 260
 DB 856 AAACCAATATTTGATGATCCGTGAGAGAC-----ACACTGGAATGGAACCTTGAAG 909
 QY 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
 DB 910 CTTTAACTATTACTGTCGAAGACAGCAATTTGGCTTTGAAGAGGCTTTAACTGTCATA 969
 QY 281 TyrThrThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
 DB 970 AATGTGATCATC-----AAAGATTCTGACCTGAAGTGGAGAGCTCACTGCTAG 1020
 QY 301 SerIleSer---HisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLys 319
 DB 1021 GCGAAAAGTATTAATCATCTTAAGAGATGAATCATTTGACCTAATATATATCTTGA 1080
 QY 320 LysValThrSerGluAspLeuLysLysSerValValCysHisAlaArgSerAlaLysGly 339
 DB 1081 AAGTCACTCAGCGTGAATCTTCCAGAGAACTTTGTTGCTTTCAGCAACTCCATTTGA 1140
 QY 340 GluValAlaLysAlaLysValLysGlnLysValProAlaProArgTyrThrValGlu 359
 DB 1141 AACACAAACCAAGTCCGCAACTGAAGAAAG-----AGAGAGTGTGCTC 1188
 QY 360 LeuAlaCysGlyPheGlyAlaThrValLeuLeuValValIleLeuIle-----ValVal 377
 DB 1189 CTGTACATCTGCTTGGACATCGGAGACCTGTGTGCGGTGCGGTGCGGTGCGGTGCG 1248
 QY 378 TyrHisValTyrTyrLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGlu 397
 DB 1249 CTCTACAGCAGCTGATTAATGATGCTGTCTGTACCGAGCTACCAAGCAAGCAAGTAC 1308
 QY 398 ThrIleLeuAspGlyLysGlnTyrAspIleTyrValSerTyrAlaArg----- 413
 DB 1309 ACCCTTGGGATTAAGAGATTTGATGCTTGTATCTTATGCAAAAGAGACTCTTTT 1368
 QY 414 -----AsnAlaGluGluGluGluPheValLeuLeuThrLeuArgGly 427
 DB 1369 CCAGTGAAGCCACTCATCTCTGAGTGAAGAACTTGGCCCTGAGCTATTTCTGAT 1428
 QY 428 ValLeuGluAsnGluPheGlyTyrLysLysCysIlePheAspArgAspSerLeuProGly 447
 DB 1429 GTTTTAGAAACAAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1488
 QY 448 GlyAsnThrValGluAlaValPheAspPheIleGlnArgSerArgArgMetIleValVal 467
 DB 1489 GGAAGTATGACAGAGACATTTGATGATTTATTAAGAGAGAGAGAGAGATTTATTC 1548
 QY 468 LeuSerProAspTyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyVal 487
 DB 1549 TTGAGCCCAACTATGTCAGAGCAACCACTTTTGAACATCAAGCAGCAGTGAATCTT 1608
 QY 488 MetCysGlnAsnSerIleAlaThrLysLeuIleValValGluTyr-----Arg 503

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Db 1609 GCCTTGATGATCA---ACACTGAAATCATTTTATTAAGTCTCTTACTTCCAGAG 1665
Qy 504 ProleuGlnIleProHisProGlyIleLeuGlnLeuLysGluSerValSerPheValSer 523
Db 1666 CCAAGACTCTTACTCATCTC---GTGAAAAAGCTCTCAGGGTTTGTGCCACAGTTACT 1722
Qy 524 TPlySGlyLysSerLysHisSerGlySerLysPheThrLysAlaLeuAla 543
Db 1723 TGGAGAGGCTTAAATACAGTCTCTCCCAATTCAGTTCGGGCCAAAATCCCTACAC 1782
Qy 544 LeuProLeuArgSerLeuSerAlaSerSerGlyTTPasnGluSerCysSerSerGlnSer 563
Db 1783 ATGCGCTGTAATAAAC---TCTCAGGAGATTCACTGGAACACAGCTCAGAAATTACTAG- 1838
Qy 564 AspIleSerLeuAspHisValGlnArgArgSerArgLeuLysGluProProGluLeu 583
Db 1839 GATTTTTCAGTGAAGAGACTCAGTAGAACAGAACCACTGGAGAGGCT-CCACAGCTTA 1897
Qy 584 GlnSerSerGluArgAlaIleGlySerPro-----ProAlaProGly***MetSerLys 601
Db 1898 AGGAATGCTGAATAGAGCCCTGAGAGCCCTCCAGTCCACTCCTGGG---ATAGAGATG 1954
Qy 602 HisArgGlyLysSerSerAlaThrCysArgCysCysValThrTyrcysGluGluAsn 621
Db 1955 TT-GCTGACAGAACTCAGAGCTCTGTGTGTGTGTCTC----- 1992
Qy 622 HisLeuArgAsnLysSerArgAlaGluIleHisasnGlnProGlnThrGlnHisLeu 641
Db 1993 AGGCTGATAGAAATTCAGAAAGACTCTCTG----- 2022
Qy 642 CysLysProValProGlnGlnSerGluThrGlnThrIleGlnasnGly 657
Db 2023 -----CCAGCACCAAGCAAGCTTGAAGCAATGG-----AATGGG 2058

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RESULT 11

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US-10-212-287-6
: Sequence 6, Application US/10212287
: Publication No. US20030003542A1
: GENERAL INFORMATION:
: APPLICANT: Sims, John
: APPLICANT: Born, Theresa
: TITLE OF INVENTION: ACPL DNA and Polypeptides
: FILE REFERENCE: 2872-US
: CURRENT APPLICATION NUMBER: US/10/212,287
: PRIOR FILING DATE: 2002-08-02
: PRIOR APPLICATION NUMBER: PCT/US99/01420
: PRIOR FILING DATE: 1999-01-22
: PRIOR APPLICATION NUMBER: 60/078,835
: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: 60/072,301
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 6
: LENGTH: 2681
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (484)..(2283)
: OTHER INFORMATION:
US-10-212-287-6

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Alignment Scores:

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Pred. No.: 7.78e-47 Length: 2681
Score: 495.00 Matches: 181
Percent Similarity: 44.25% Conservative: 127
Best Local Similarity: 26.01% Mismatches: 288
Query Match: 13.49% Indels: 104
Db: 9 Gaps: 27

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US-10-061-727-2 (1-687) x US-10-212-287-6 (1-2681)

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Qy 11 TyrPheTyrGlyIleLeuInSerAspAlaSerGluArgCysAspAspTrpGlyLeuAsp 30
Db 503 TATTTCTTTGGCTGTGTGTGAGGA-GAGCGAATTTAAAGATTAAATTTCCAGGTGTCC 561
Qy 31 ThrMetArgGlnIleGlnValPhe-----GluAspGluProAlaArgIleLysCys 47
Db 562 ACAAAAATACTCTTGGACATATTTCTACAGAGAGTGAAGAGAAATTTGTTATTATTGT 621
Qy 48 ProLeuPheGlu-----HisPhe----- 53
Db 622 GATTTACAGAGCCAGCAAAATCACATTTCTGCCACAGAAATGACTCTACCAAAAACA 681
Qy 54 -----LeuLysPheasnTySerThrAlaHisSerAlaGlyLeuThrLeuIle 69
Db 682 GTCCCTGAGACACTGCCCTTCAATGGTAGTAAGACACTATCT-----GATGTCCAA 732
Qy 70 TrpTyTrpThrArgGlnAspArgAspLeuGluProIleAsnPheArgLeuProGlu 89
Db 733 TGGTACCAACAACCTTCGAATGAGATCCATTAGAGACATTAGAAAGCTATCTCT--- 789
Qy 90 AsnArgIleSerLysGluLysAspValLeuTrpPheArgProThrLeuLeuAsnAspThr 109
Db 790 ---CACATCATTCAGCAAAATGTACCTTCACTTTTGAACCCAGGGGTGAATTAATCT 846
Qy 110 GlyAsnTyThrCys-----MetLeuArg-----AsnThrTyrcysSer 123
Db 847 GGGTCAATATATTTGTGAGCCCAAGATGATTAAGAGCCCTATGATATACCTGTGTGTC 906
Qy 124 LysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSerProMetLys 143
Db 907 AAGATGATTTTAAAGTTAAGTGAAGCCCAAGAAATGATCTGTGAGATTCGGCATCA--- 963
Qy 144 LeuProValHisLeuLeuTyrlleGlyTyrgly---IleGlnArgIleThrCysProasn 162
Db 964 -----CATAGCAAGAACCTTACTTCTGGAGCACTGCTCATATTTCTGCCCACT 1014
Qy 163 ValAspGlyTyrcysPheProSerSerValLysProThrIleThrTrpTyrcysGly----- 180
Db 1015 CTCAGCTGCCAA---AGTAGACCAAAAGTCCAGCGTACCTGGTACAGAAATGAGAAA 1071
Qy 181 CysTyrlleGlnIleAsnAspAsnValIleProGluIleMetCysLeuSerPheLeu 200
Db 1072 CTCCTCTGTGTGAAGAGCAAGCAACGAATCGTAGTAGAAGTT----- 1116
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrcysValValThrTyrcysProGluasnGly 220
Db 1117 -----TATGACTATCACAGGCGACATATGTATGTGATTACACTCAGTCGATACTGTG 1170
Qy 221 ArgThrPheHisLeuThrArgThrIleuThrValIleValValGlySerProLysAsnAla 240
Db 1171 AGTTGCTGACAGCTCAGAGCTGTGTTCAGAGTAGAACCAATGTGGAGACACTAAACTC 1230
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Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleasnGlu 300
Db 1345 AAATGTACATC-----AAAGATTCTGACCTTAGAGTGGAGCTTCAGACTGAG 1395
Qy 301 SerIleSer---HisSerArgThrGluAspGluThrArgThrGlnIleLeuSerLys 319
Db 1396 GCGAAAGATTTAAATCACTTAAGATGAATATGATGAGGTATATATCTTTGGAA 1455
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Db 1456 AAAGTCACTCAGCGGTGATCTTCGACAGAAAGTTGTGCTTGTCCAGAACTCCATTGGA 1515

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Page 14

	APPLICANT: Mohler, Kendall M.	
	APPLICANT: Born, Teresa L.	
	TITLE OF INVENTION: METHODS FOR TREATING IL-18 MEDIATED DISORDERS.	
	FILE REFERENCE: 3086-A	
	CURRENT APPLICATION NUMBER: US/09/981,421	
	CURRENT FILING DATE: 2001-10-17	
	PRIOR APPLICATION NUMBER: US 60/241,408	
	PRIOR FILING DATE: 2000-10-18	
	NUMBER OF SEQ ID NOS: 5	
	SOFTWARE: PatentIn version 3.1	
	SEQ ID NO 1	
	LENGTH: 2681	
	TYPE: DNA	
	ORGANISM: Homo sapiens	
	FEATURE:	
	NAME/KEY: CDS	
	LOCATION: (484)..(2283)	
	OTHER INFORMATION:	
	US-09-981-421-1	
Alignment Scores:		
Pred. No.:	7,78e-47	Length: 2681
Score:	495.00	Matches: 181
Percent Similarity:	44.25%	Conservative: 127
Best Local Similarity:	26.01%	Mismatches: 288
Query Match:	13.49%	Indels: 104
DB:	10	Gaps: 27
US-10-061-727-2 (1-687) x US-09-981-421-1 (1-2681)		
QY	11 Tyrhetyrglyleleuglnseraspalasergluargcysaspaprtprglyleuasp	30
DB	503 TATTTCTTGCGCTTGTCGAGGA-GAGCGAATTAAGATTTAATATTCAGTTGTCC	561
QY	31 Thmetargtlnleluvalphe-----Glusplulpralargilelys	47
DB	562 ACAAAAACCTCTTGACATATTTCAAGAGAGTGAGAGAAATTTGCTATTTTGT	621
QY	48 Proleuhgu-----Hisphe-----	53
DB	622 GATTACACAGGCCACAGAAATCAATTTCTGCCACAGAAATGACTCTACCAAAACA	681
QY	54 -----leuylspheasnyrserthralhisseralaglyleuthleuile	69
DB	682 GTCCGTGAGACCTGCCCTTCATGGGTATGACGACTACT-----GATGTCAA	732
QY	70 TrpTyrrtrphrarglnaspaargaspueugluProilleasnpheargyleuProglu	89
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QY	90 AsnargliserlysgulysaspvalleutrpPheargrprothrleuLeuAasapthr	109
DB	790 ---CACTACATTCAGCAAAATGTACCTTCACCTTTTGAACCCAGGGGTAATATCT	846
QY	110 Glyasnrytrthrcys-----Metleuarg-----AsnthrThyrcysSer	123
DB	847 GGGTCATATATTTGTATACACCAAGATGATTAAGACGCCCTATGATGAGCGCTGTGTGC	906
QY	124 LysValAlaheproleugluvalalginlyaspserycysPheasnserrProthelys	143
DB	907 AAGATGATTTTGAAGATTAAGCCCAAGACAAATGATCTCGTATGATATTCGCCATCA--	963
QY	144 LeuproValHislylseuTyrlleuglytyrGly---lleAlnargllethrcysProasn	162
DB	964 -----CATTAAGCAAGACCTTACTTTGGAGCACTGGCTCTATTTCTTCCGCCAAGT	101
QY	163 ValAspGlytyrPheproSerSerValysProthrIlethTrpTyrmetyly-----	180
DB	1015 CTCAGCTGCCA---AGTATGCAACAAGTCAAGCGGTATACCTGTATCAAGAATGAGAAA	107
QY	181 CysTyrllylleglinsnphasnasnValilleProgluGlymecasnleuserPheleu	200

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/924,777
 FILING DATE: 2000-01-31
 APPLICATION NUMBER: US 07/963,928
 FILING DATE: 20-OCT-1992
 APPLICATION NUMBER: US 08/027,750
 FILING DATE: 08-MAR-1993
 APPLICATION NUMBER: US 08/183,563
 FILING DATE: 18-JAN-1994
 APPLICATION NUMBER: US 08/381,603
 FILING DATE: 27-JAN-1995
 APPLICATION NUMBER: US 08/567,710
 FILING DATE: 05-DEC-1995
 APPLICATION NUMBER: US 08/685,212
 FILING DATE: 23-JUL-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Bastian, Kevin L.
 REGISTRATION NUMBER: 34,774
 REFERENCE/DOCKET NUMBER: 018484-002280US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1782 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 46..1776
 OTHER INFORMATION: /product= "mouse interleukin-1 receptor"
 US-09-731-175-3
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-10-061-727-2 (1-687) x US-09-731-175-3 (1-1782)
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 Pred. No.: 6,47e-46 Length: 1782
 Score: 484.50 Matches: 153
 Percent Similarity: 46.04% Conservative: 120
 Best Local Similarity: 25.80% Mismatches: 225
 Query Match: 13.21% Indels: 95
 DB: 10 Gaps: 27

160 CysProAsnValAspGlyTyrPhe-----ProSerSerValLysProThrIleThrTrp 177
 478 TCCCTTATATGTC---AGTATATTTAAAGTAAATTAATAGACTACCCGAGGCTCCAGTGG 534
 178 TyrMetGlyCysTyrLysIleGlnAsnPheAsnAsnValIleProGlnGlyMetAsnLeu 197
 535 TYTAAGAACTGT---AAACCTCGCTTCTTGACAAAGTAAAGCTTCTTGAGTAAAGAT 591
 198 SerPheLeuIleAlaLeuIleSer-----AsnAsnGlyAsnTyrThrCysValValThr 215
 592 AAACGTGTGTGAGCAAGATGTGCTGTAAGACACAGAGGAGCACTATATATGCGTATGTC 651
 216 TyrProGlnAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysValValGly 235
 652 TATAGCTTCCGGGGAGAGCAATATCCGGTCAACAGGTAAATCAATTTATCAATATAGAT 711
 236 SerProLysAsnAlaValProProValIleHisSerProAsnAspHisValValTyrGlu 255
 712 GAAACAAAGAGGAGC---AGACCTGTATCTCGAGCCCTCGGAATGAGAGATC---GAA 765
 256 LysGluProGlyGlnGluLeuLeuLeuProCysThrValTyrPheSerPheLeuMetAsp 275
 766 GCTGACCCAGGATCAATGTATTAACACTGATCTCAACGTAACGAGCCAGTTC----- 816
 276 SerArgAsnGluValTrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAsp 295
 817 ---TCAGACCTGTCTACCTGAGAGTGAATGATCA-----GAA 852
 296 ValThrIleAsnGlnSer-----IleSerHisSerArgThr 307
 853 ATGAATGAGAAATGATATCCATTTCTAGCTGAAGACTATCAATTTGTGGAAATCTTCAACC 912
 308 GluAspGlu---ThrArgThrGlnIleLeuSerIleLysLysValThrSerGluAspLeu 326
 913 AAAAGAAATACACACTCATTAACAACACTTTCAGAGTTTAAAGCTTAAAGAGCTTTAT 972
 327 LysArgSerTyrValCysHisAlaArgSerAlaLysGlyValAlaLysAlaLys 346
 973 CGCTATCCGTTATATCTGTGTGTGTAAAGACAC---AAATTTTGAATCGGGCAT 1026
 347 ValLysGlnLysValProAlaProArgTyrThrValGluLeuAlaCysGlyPheGlyAla 366
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 367 ThrValLeuLeuValValIleLeuIleValValTyrHisValTyrTrpLeuGluMetVal 386
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 387 LeuPheTyrArgAlaHisPheGly-----ThrAspGluThrIleLeuAspGlyLysGlu 404
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 405 TyrAspIleTyrValSerTyrAlaArgAsnAlaGluGlu-----Glu 418
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 439 IlePheAspArgAspSerLeuLeuProGlyGlyAsnThrValGlnAlaValPheAspPheIle 458
 1327 ATTATAGAGAGGATGATCTATGTGTGAGAGATACCATGAGGTTTCTATATGAATAATGTA 1386
 459 GlnArgSerArgMetIleValValLeuLeuSerProAsp----- 471
 1387 AGAAGAAAGCAGAGAGCTATATATCTTATGAGAGATATAGGAGAGCTTCAAGCTGCTG 1446
 472 ---TyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyValMetCysGln 490
 1447 GGCAGATCATCTGAGAGAGCAATATAGCCATA-----TACAATGCTTCATTCACAG 1494

GenCore version 5.1.4 ps 4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: April 30, 2003, 09:52:34 ; Search time 1672 Seconds

(without alignments)
6654.485 Million cell updates/sec

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Perfect score: 3669
Sequence: 1 MTLWCVSVLYFYGILOSDA.....SALALHHFTLSNNNDFFYL 687

Scoring table:
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-O=/cgn2_1/USPTO_spool/US10061727/runat_23042003_083116_7900/app_query.fasta_1.839
-DB=EST -QFMT=fastap -SUFFIX=1st -MINMATCH=0.1 -LOOPEXT=0 -LIST=45
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -MODE=LOCAL
-DOCALIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NOMM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10061727@cgn2_1.1456@runat_23042003_083116_7900 -NCDU=6 -TCPU=3
-NO XLPXY -NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -LONGLOG -DEV TIMECUT=120
-WARN TIMECUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
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1: em_estba:
2: em_esthum:
3: em_estin:
4: em_estmu:
5: em_estrov:
6: em_estrpl:
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8: em_hic:
9: gb_est1:
10: gb_est2:
11: gb_hic:
12: gb_est3:
13: gb_est4:
14: gb_est5:
15: em_estfun:
16: em_estom:
17: gb_ggs:
18: em_ggs_hum:
19: em_ggs_inv:
20: em_ggs_pin:
21: em_ggs_vrt:
22: em_ggs_fun:
23: em_ggs_mam:
24: em_ggs_mus:
25: em_ggs_othet:
26: em_ggs_pro:
27: em_ggs_rod:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result. No.	Score	Query Match	Length	DB ID	Description
1	1865	50.8	1549	11 BC016141	BC016141 Homo sapi
2	1289	35.1	849	9 AL543511	AL543511 AL543511
3	1281	34.9	873	13 B1862501	B1862501 603390624
4	1277	34.8	880	13 B1330085	B1330085 602982187
5	1124	30.6	814	14 B0006059	B0006059 UI-H-E11-
6	1012	27.6	723	10 AW211290	AW211290 uc079b07.y
7	999	27.2	756	9 A1303998	A1303998 ui63d12.y
8	989	27.0	888	13 B1331848	B1331848 602982528
9	927	25.3	910	12 BE892231	BE892231 601435065
10	915	24.9	580	13 B1346913	B1346913 376288 MA
11	900	24.5	596	10 AV656295	AV656295 AV656295
12	876	23.9	489	14 BM760155	BM760155 K-EST0040
13	873.5	23.8	588	9 AA237107	AA237107 mw96b02.x
14	863	23.5	789	10 AV659167	AV659167 AV659167
15	858	23.4	652	10 BB625831	BB625831 BB625831
16	853	23.2	533	9 AA239486	AA239486 mw98g02.x
17	834	22.7	643	10 BB626271	BB626271 BB626271
18	834	22.7	676	10 BB653335	BB653335 BB653335
19	817	22.3	643	9 AA107505	AA107505 mp05d08.x
20	807.5	22.0	885	12 BF237012	BF237012 602026645
21	805	21.9	646	10 BB612046	BB612046 BB612046
22	784	21.4	923	9 AL544533	AL544533 AL544533
23	769	21.0	500	9 AA571281	AA571281 V190903.x
24	766	20.9	616	10 AV661936	AV661936 AV661936
25	766	20.9	637	10 BB623025	BB623025 BB623025
26	700	19.1	475	14 B0561650	B0561650 B4671902-
27	687	18.7	545	10 BB633613	BB633613 BB633613
28	685.5	18.7	632	13 B1065068	B1065068 p9E1n.pk0
29	685	18.7	644	9 AA819412	AA819412 UI-R-A0-b
30	675	18.4	537	13 B1340158	B1340158 365346 MA
31	656	17.9	396	14 T082717	T082717 EST06168.in
32	625	17.0	567	14 BM751599	BM751599 K-EST0027
33	602.5	16.4	586	12 BG711109	BG711109 p9J1n.pk0
34	587	16.0	355	10 AV654169	AV654169 AV654169
35	570.5	15.5	938	12 BG032519	BG032519 602301430
36	569	15.5	850	13 B1872969	B1872969 603398140
37	536	14.6	392	10 AA427989	AA427989 64724 MAR
38	497.5	13.6	426	14 T70863	T70863 yd15f12.r1
39	497.5	13.6	570	14 H80590	H80590 yu76e04.x
40	494.5	13.5	560	13 B1065233	B1065233 p9E1n.pk0
41	488.5	13.3	712	13 B1106737	B1106737 602891267
42	471	12.8	520	9 A1529899	A1529899 ui83g06.y
43	466	12.7	415	10 BB644209	BB644209 BB644209
44	426	11.6	305	10 AA485290	AA485290 64805 MAR
45	394.5	10.8	309	14 T85756	T85756 yd60e03.r1

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE
BC016141	BC016141	Homo sapiens, interleukin 1 receptor accessory protein, clone IMAGE:3920152, mRNA.	BC016141	BC016141.1	GI:16359373	Homo sapiens.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	Strausberg, R.	Direct Submission
1549 bp	mRNA	linear	HTC 24-OCT-2001							

Db 180 ATGATATGCGATTGAGAGATCACTTGCCAAATGATGATATTTCCCTCAGT 239

Qy 171 VallysProthrlleThrTryptylmetGlyGlyTylsIleGlnasnPhenasnVal 190

Db 240 GTCAACCGACTATGACTGTATATGAGGCTGTATATAATACAGAAATTTATATATGA 299

Qy 191 TleProgluGlyMetasnleuSerPheleuIleAlaIleuIleSerasnngIlyAsnTyr 210

Db 300 ATACCGAAGGATATGAACTTGAGTTCCTCATGTCCTTAATTTCAATATATGAAATTAAC 359

Qy 211 ThrCysValIleValThrTyrProgluasnGlyArgThrPheHisleuthrArgThrLeuthr 230

Db 360 ACATGTGTGTATACATATCCAGAAATGACGATGCTTCATCTCCAGGACTGACT 419

Qy 231 VallysValIleGlySerProlysaAsnAlaValProProValIleHisSerProAsnAsp 250

Db 420 GTAAAGTAGTAGGCTCTCAAAAATGACAGTCCCTGTGTATCCATTCACCTATATGAT 479

Qy 251 HisValIleValTyrGlnIleGluProgluIleuIleuIleuIleProCysThrValTyrPhe 270

Db 480 CATGTGCTATGAGAAACACGAGAGAGACTACTATTCCTGTACGGCTATATTTT 539

Qy 271 SerPheLeuMetAspSerArgasnGluValTryptThrIleAspGlyTylsIleProAsp 290

Db 540 AGTTTCTGATGATGATTTCTGCAATGAGCTTTGGTGACCATTCATGATGAAAAAAGCTGAT 599

Qy 291 Aspilethrlle-AspValThrIleasnGluSerIleSerHisSerArgThrIleAspGly 310

Db 600 GACATCATATGATGATGATTCACCATTTACGAAATATATGATATGATGATGATGATGAT 659

Qy 310 V-ThrArgThrGlnIle-IleuSerIleIys-IysValIleThrSerGluAsnLeuIleArgse 329

Db 660 AAACAGAACTGACATTTTGTAGACATCAAGAAAGTACTCTGAGAGATCTCAAGGGCAG 719

Qy 329 TTYrValCysHisAlaArg-SerAlaIleGlyGluVal-AlaIleValIleValIleValIle 348

Db 720 CTATGTCTCTATGCTAGAGGGGTCCAAAGCGGAACTTTCGCAAGCACCGAAGGTGAAG 779

Qy 349 GlnIys 350

Db 780 CAGAAA 785

RESULT 4

LOCUS B1330085 880 bp mRNA linear EST 30-JUL-2001

DEFINITION 602982187P1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:5135061 5',

ACCESSION B1330085

VERSION B1330085.1 GI:15014755

KEYWORDS EST.

ORIGIN

ORGANISM

Mus musculus.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 880)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: rgs@bimail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNT)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNT, at: http://image.lim.gov

Place: LHM1331 row: n column: 22

High quality sequence start: 3

High quality sequence stop: 870.

Location/Qualifiers

1..880

source

location="Mus musculus"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:5135061"

/clone_id="NCI_CGAP_L19"

/lab_host="DH10B (T1 phage-resistant)"

/note="Organ: liver; Vector: pCMV-SPORE; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP library."

BASE COUNT 249 a 215 c 193 g 223 t

ORIGIN

Alignment Scores:

Pred. No.: 2,536-125 Length: 880

Score: 1277.00 Matches: 242

Percent Similarity: 91.22% Conservative: 28

Best Local Similarity: 81.76% Mismatches: 23

Query Match: 34.81% Indels: 6

DB: 13 Gaps: 0

US-10-061-727-2 (1-687) x B1330085 (1-880)

Qy 46 LysCysProleuPheGluHisPheleuIysPheasnTyrSerThrAlaHisSerAlaGly 65

Db 1 CAGTCCCTCCCTCTTTGAACTCTCTGAGATGACATACAGACATGCGCATTTCTCTGCG 60

Qy 66 LeuthrleuIleTyrTyrTryptThrArgGlnAspArgAspLeuGluProIleasnPhe 85

Db 61 CTACCTGATCTGGATCTGATGACCGACGACACCGGACCTGAGAGACCATTAATTC 120

Qy 86 ArgLeuProGluAsnArgIleSerIleGlnIysAspValIleThrPheArgProthrlleu 105

Db 121 CGCTCCCAAGAAATCGATCATGAGGAGAAAGTGTCTGTCTGCTCCGACCCCTC 180

Qy 106 LeuAsnAspThrIleGlyAsnTyrThrCysMetLeuArgAsnThrIleTyrCysSerIysVal 125

Db 181 CTCATATGACACCGGAAATTAACCTGCATGTGAGGAACAACAATTAATGACGAAAGTT 240

Qy 126 AlaPheProleuGluValIleGlnIysAspSerCysPheAsnSerProMetIysLeuPro 145

Db 241 GCATTTCCCTGGAAGTGTTCAGAAAGACAGCTGTTCATTTCCATGACATGATTCACA 300

Qy 146 ValHisIysLeuTyrIleGluTyrGlyIleGlnArgIleThrCysProAsnValAspGly 165

Db 301 GTGCAACAGATGATATTAAGAACATGCACTTAATGATCAATGATCCAAATGTACACGA 360

Qy 166 TyrPheProSerSerValIysProthrlleThrTryptIleMetGlyCysTylsIleGln 185

Db 361 TACTTCTCTTCCAGTGTCAACATGCAATCGGTCACTTGATTAAGGGTGTACTGAATATG 420

Qy 186 AsnPheAsnValIleProgluIleMetasnleuSerPheleuIleAlaIleuIleSer 205

Db 421 GACTTCAATATGATACACCGAGGGACATGAACTTGACCTTTTCATCTCCCTGTGATCA 480

Qy 206 AsnAsnIysAsnTyrThrCysValIleThrTyrProgluAsnGlyArgThrPheHisleu 225

Db 481 AATAACGAAATTAACATGATGTGTATCATATCTGAAAACGAGCTCTTTACCTC 540

Qy 226 ThrArgThrLeuthrValIysValIleGlySerProlysaAsnAlaValProProValIle 245

Db 541 ACCAGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 599

Qy 246 HisSerProAsnAspHisValIleValIleGlnIysGluProgluIleGluLeuIlePro 265

Db 600 TATTTCCAAATGACCGGTGTGTATAGAAAGAACACGAGAGGAACTGTATTTCC 659

Qy 266 CysThrValTyrPheSerPheleuMetAspSerArgasnGluValIleTryptThrIleAsp 285

Db 660 TGCAAAGTCTATTTCAATTTATGATGATGATGATGATGATGATGATGATGATGATGAT 719

Qy 286 GlyIysIysProAspAspIleThrIleAsp-ValThrIleasnGluSerIleSerHisle 305

Db 720 CGAAAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 779

Qy	305	ra3grhr--GuasgsgluthArqthrglnlieuserrileyslysva1Thserrglu 324
Db	780	TTTACCCGAGAAAGATGAAACCAAGCAGCTAGATTGAGACATCAAGAAAGTACACCCCGAG 839
Qy	325	AspleulyaArgSerTyTValCysHisAlaIaArgSerAlaTyS 338
Db	840	GATCC-TCAGGGCAATATGTCTGTCA-CCTCGAATATACCAAG 879
RESULT 5		
BQ006059/c		BQ006059/c
LOCUS		814 bp mRNA linear EST 26-MAR-2002
DEFINITION		UI-H-E11-ayz-f-07-0-UI.s1 NCI CGAP_E11 Homo sapiens CDNA clone
ACCESSION		IMAGE:5845638 3', mRNA sequence.
VERSION		BQ006059
KEYWORDS		BQ006059.1 GI:19730959
TRACE		EST.
RGANISM		human.
ANCESTRY		Homo sapiens
LOCUS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DEFINITION		Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
ACCESSION		1 (bases 1 to 814)
VERSION		NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
KEYWORDS		National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TRACE		Tumor Gene Index
RGANISM		Unpublished (1997)
ANCESTRY		Contact: Robert Strausberg, Ph.D.
LOCUS		Email: cgapbs-remail.nih.gov
DEFINITION		Tissue Procurement: Dr. Jose Mercuende
ACCESSION		CDNA library preparation: Dr. M. Bento Soares, University of Iowa
VERSION		CDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
KEYWORDS		DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
TRACE		Clone Distribution: Clone distribution information can be found
RGANISM		through the I.M.A.G.E. Consortium/LNLB at: http://image.llnl.gov
ANCESTRY		The following repetitive elements were found in this CDNA
LOCUS		sequence: 79-186, >ALU (matched complement)
DEFINITION		Seq primer: M13 FORWARD
ACCESSION		POLYA=Yes.
VERSION		
KEYWORDS		
TRACE		
RGANISM		
ANCESTRY		
LOCUS		
DEFINITION		
ACCESSION		
VERSION		
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LOCUS		
DEFINITION		
ACCESSION		
VERSION		
KEY		

DB:	0	14	Gaps:	0
US-10-061-727-2 (1-687) x BQ006059 (1-814)				
Qy	138	PheasnsErProMeTylsleuProValHisIeIysleuTyrlIeGlutYrGlyIleGlnArg	157	
Db	814	TTCAATTCCTCCCATGAAACTCCAGTGCATAACTGATATAGAAATATGNAATTCAGAGG	755	
Qy	158	IlleHrCysProAsnValIarPglYrPhrProSerSerValysProThrIleThrTrp	177	
Db	754	ATCACTGTGCCAAATATGATGATGATATTTCTTCAGGTCTAAACCGACTATCATCTGG	695	
Qy	178	TyrMetGlyCysTrpIlysiIleGlnAsnPhesAsnValIleProGluGlyMetAsnIleu	197	
Db	694	TATATGGCTGTTTATAAATACAGAAATTTATATATATATATACCGAAGTATGAAGCTTG	635	
Qy	198	SerPheIleuIleAlaIleuIleSerAsnAsnGlyIAsnTrpThrCysValValThrTyPro	217	
Db	634	AGTTTCCTCATTCGCTTAATTTCAATAATATGAAATTCACATGCTGTGTACATATCCA	575	
Qy	218	GluAsnGlyIatGrThrPheHisIleuThrArgThrIleuThrValIysValValIglYserPro	237	
Db	574	GAAATATGACCTATGCTTTCATCTCACAGAGACTCTGACTTAAGATGATGAGCTTCCA	515	
Qy	238	LysAsnIleValIleProProValIleHisSerProAsnAspHisValValTyrgIuYsGlu	257	
Db	514	AAAAATGACAGTCCCTCGATCATCTTCACTATATATATATATATGCTATGAGAAAGAA	455	
Qy	258	ProGluGluGluIleuIleProCysThrValTyPheSerPheIleuMetAspSerArg	277	
Db	454	CCAGAGAGAGAGCTACTCATCTCCCTGTACGGTCTATTTAGTTTTCATGATGATTCGCG	395	
Qy	278	AsnGluValIleTrpTrpThrIleAspGlyIyIysIyProAspAspIleThrIleAspValThr	297	
Db	394	AATGAGTTTGTGTGACCATTTGATGAAAAAAMACCTATATGACATCTATTTGATGATCACC	335	
Qy	298	IleAsnGluSerIleSerHisSerArgThrGluAspGluThrArgTrgIleIleuSer	317	
Db	334	ATTAACGAAATGATATAGTCATATGATGAGACAGATATGAAACAGAACTCAGATTTTGAGC	275	
Qy	318	IleIyIysValIleThrSerGluAspIleuIysAspSerTyValCysHisIleArgSerIleA	337	
Db	274	ATCAGAAAGTTTACTCTCGAGGATCTCAAGCGCAGCTATATGCTGTCAATGATGAGTCC	215	
Qy	338	LysGlyIuValAlaIyIysValIyIysValIySgIuIys	350	
Db	214	AAAGCGAAGTTGCCAAAGCAGCAGGAGTGAGCAGCAGAG	176	
RESULT 6				
AW211290		723 bp	linear	EST 03-DEC-1999
LOCUS				
DEFINITION		uc079b07.y1 NCI CGAP Mam3 Mus musculus cDNA clone IMAGE:2648725 5'		
VERSION				
KEYWORDS		similar to gb:X65995 M.musculus mRNA for interleukin 1 receptor		
SOURCE		accessory (MOUSE);, mRNA sequence.		
ORGANISM		AW211290		
		AW211290.1	GI:6517238	
		EST.		
		house mouse.		
		Mus musculus		
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus-		
		1 (bases 1 to 723)		
		NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .		
		National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
		Tumor Gene Index		
		Unpublished (1997)		
JOURNAL		Contact: Robert Strausberg, Ph.D.		
COMMENT		Email: cga@bbs-remail.nih.gov		
		Tissue Procurement: Lochar Hennighausen Ph.D., Chu-Xia Deng Ph.D.		
		cDNA Library Preparation: Life Technologies, Inc.		
		cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNU)		
		DNA Sequencing by: Washington University Genome Sequencing Center		
		Clone distribution: NCI-CGAP clone distribution information can be		

Page 6

QY	209	AsnYrTrhYsValValThlYrProGluSngIYAgrThrPheHlEleuthrArgThr	225
Db	2	AATTCACAGTGTGGTTACATATCTCTGAAACGAGCCTCTTTCACCTCACCGAGACT	61
QY	229	LeuthrValLysValValIGlySerProLysSnnalValProProValIlHlHisSerPro	245
Db	62	GTGACTGTAAAGTGGTGGGCTCACCAAGAGATGCATTTGGCCACCCAGATCATTTCTCCA	122
QY	249	AsnAspHisValValYrGlyLysGluProGlyGlyGluLeuLeuIleProCysThrVal	265
Db	122	AATGACCGTGTGTCTTAAGAAAGAACCCAGAGAGGAGACTGGTATATCCCTGCAAGATC	187
QY	269	TyrPheSerPheLeuMetAspSerArgSngIuValTyrPTrPThrIleAspGlyLysLys	285
rh	182	TATTCAGTTCATATATGATGACTCCCACAATGAGGGCTGGTGACCATTTAGTGAAGAAG	241
QY	289	ProAspAspIleThrIleAspValThrIleSngIuSerIleSerHisSerArgThrGlu	305
Db	242	CCTGATGACGTCACAGTGCATCATCATTAATAGAAGTGAATTTTCTTCAACCGAA	301
QY	309	AspGluThrArgThrGlnIleLeuSerIleLysLysValThrSerGluAspLeuLysArg	325
Db	302	GATGAACCAAGACATCGATTTTGGCATCAAGAAAGGCACCCCGAGCATCTCAGCC	361
QY	329	SerYrValCysHisAlaArgSerAlaLysGlyGluValAlaLysAlaAlaLysValLys	345
Db	362	AACATATGCTGTCAATGCTCGAAATACCAAGAGGAGACCTGAGCGCTGCCAAGGTGAA	421
QY	349	GlnLysValProAlaProArgYrThrValGluLeuAlaCysGlyPheGlyAlaThrVal	365
Db	422	CAGAAAGCATACCAACCAAGGTACACAGTGAACCTCCCTGTGTATYAGAGCCACGCT	481
QY	369	LeuLeuValValIleLeuIleValValYrHisValYrTrpLeuGluMetValLeuPhe	385
Db	482	TTTCTGTGTAGGTGTCTCATTTGTGTGTATTCACATGTATACGTGAGAGATGTCCTCTT	541
QY	389	TyrArgAlaHisPheGlyThrAspGluThrIleLeuAspGlyLysGlyLysTyrTrpAllyr	405

QY	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Db	542	TACGAGCTCACTTGGAGACAGATGAGCAATTCCTGATGGAAGAGATGATATATTAT	601								
QY	409	ValserTyrralabAgsena1agiuglugluGluPhelAlleuLeuthr-leuargtgiVa	428								
Db	602	GTATGCTATGACACACATGTCGAGAGAGAAATTTTGGCTGATGAGCGCTGGCTGAAGT	661								
QY	428	1leugluAgsnluPheg1TyrrysleuCyS11lepeasparApsSerleuProglgi	448								
Db	662	CATGGAATGAGATTGGATCCAGCTGGC-ATCTTCAGACGATACCGCTGCTGGGGG	720								
QY	448										
Db	721	A 721									
RESULT 7											
AL103998											
LOCUS											
DEFINITION											
AL103998											
ACCESSION											
VERSION											
KEYWORDS											
SOURCE											
ORGANISM											
house mouse.											
Mus musculus											
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;											
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.											
1 (bases 1 to 756)											
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,											
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,											
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,											
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and											
Waterston,R.											
The WashU-HMNI Mouse EST Project											
Unpublished (1996)											
Contact: Marra M/Mouse EST Project											
WashU-HMNI Mouse EST Project											
Washington University School of Medicine											
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108											
Tel: 314 286 1800											
Fax: 314 286 1810											
Email: mouseest@watson.wustl.edu											
This clone is available royalty-free through LNL; contact the											
IMAGE Consortium (info@image.lnl.gov) for further information.											
MG1:971419											
Seq primer: custom primer used											
High quality sequence stop: 345.											
Location/Qualifiers											
1..756											
/organism="Mus musculus"											
/strain="C57BL"											
/db_xref="taxon:10090"											
/clone="IMAGE:1887095"											
/clone_id="Sugano mouse liver mlia"											
/sex="Female"											
/dev_stage="adult"											
/lab_host="DH10B"											
/note="Organ: liver; Vector: pME18S-FL3; Site 1: DraIII											
(CACTGTGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA											
was primed with an oligo(dT) primer											
(ATGTCGCTTTTATTTTATTTT); double-stranded cDNA was											
ligated to a DraIII adaptor (TGTGGCGCTACTG), digested											
and cloned into distinct DraIII sites of the pME18S-FL3											
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should											
be used to isolate the cDNA insert. Size selection was											
performed to exclude fragments <1.5kb. Library											
constructed by Dr. Sumio Sugano (University of Tokyo											
Institute of Medical Science). Custom primers for											
sequencing: 5' end primer CTCTGCTCTTAAGAAGTGGC and 3' end											
primer CGACCTGCAGCTGACACAC.											
FEATURES											
source											
199 a 185 c 167 g 195 t 10 others											

Qy 161 Pro-AsnValAspGlyTyrPheProSerValIysProThrIleThrTrpIleMetG1 180
Db 600 CCAAAATGATGACGAACTTCTTCTTCACTGATCAACCACTGCTGATTAAGG 639
Qy 180 YQSYTYLSEILGLASnDheAsnValIleProGluGlyMetAsnLeuSerPhe 200
Db 660 TTGTACTGAATATGATGACTTTCAT -AATGATACACCGAGGCGATGAACTTGAGCTTTC 718
Qy 200 uileAlaLeuIleSerAsnValIleProGluGlyMetAsnLeuSerPhe 219
Db 719 -ATCCCTTGTTGATCAATACG -AACTACACATGTTGTTTACCAATATCTTGAAA 776
Qy 219 nglYargThrPheHisIleuThrArgThrLeuThrValIleValGlySerProIysAs 239
Db 777 CGGAGACGTCCTTTCACCTCACAGATGACTGTAGG---TTGTGTATCCAAAGCA 833
Qy 239 nAlaValProPro 243
Db 834 ATGCTGCCCCCA 846
RESULT 9
992231
US BE892231 910 bp mRNA linear EST 20-OCT-2000
--FINITION 601435065F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3920152 5',
ACCESSION BE892231
VERSION BE892231.1 GI:10352355
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 910)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC/DCID/DP
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
Cloning Strategy: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
http://image.llnl.gov
Plate: LLM9751 row: a column: 17
High quality sequence stop: 710.
Location/Qualifiers
1..910
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3920152"
/clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NCI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

Qy 183 ATGACACTTCTGTGTTGTTGATGAGTCTTACTTATGAAATCTGAAATGATGCG 242
Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db 243 TAGAAGCGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 302
Qy 41 GluProAlaArgIleIleGlySerProLeuPheGlnIlePheLeuIlePheLeuIleSerThr 60
Db 303 GAGCAGCGCTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 362
Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTrpIleTrpThrArgGlnAspArgAspLeuGlu 80
Db 363 GCCCATTAAGCTGGCTTACTGATCTGATGATGATGATGATGATGATGATGATGAT 422
Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLeuGlyAspValLeuTrp 100
Db 423 GAGCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 482
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTrpIleCysMetLeuArgAsnThr 120
Db 483 TTCCGCGCCACTCTCTCAATGACACTGCACTATACCTGATGTTAGGAACACTACA 542
Qy 121 TyrCysSerIleValAlaPheProLeuGluValIleGlnIleAspSerCysPhe-AsnSe 140
Db 543 TATGACGCAAGTT -GCAATTCCTTGGAGTTGTTCAAAAGACAGCTGTTCAAAATTC 601
Qy 140 rPrometLysLeuProValHisIleLeuLeuIleGluTrp-GlyIleGlnArgIleThr 159
Db 602 CCCCATGAAGCTCCAGTGCATTAACCTGATATGAAATATGGATTCAGAGATCACT 661
Qy 160 CysProAsnValAspGlyTyrPheProSerValIysProThrIleThrTrpIleMet 179
Db 662 TGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Qy 180 GlyCysTyrIleGlnAsnDheAsnValIleProGluGlyMetAsnLeuSerPhe 199
Db 721 GCGTGTATTAATATGACGATTTTC----- 744
Qy 200 LeuIleAlaLeuIleSerAsnValIleProGluGlyMetAsnLeuSerPhe 219
Db 745 -----ATATGATATCCGAAGTT 762
Qy 220 GlyArgThrPheHisIleuThrArgThrLeuThrValIleValGlySerProIysAsn 239
Db 763 GACCTGAGTCCATGCTTAAATGACATTATGATGATGATGATGATGATGATGATGAT 822
Qy 240 AlaValProProValIleHis 246
Db 823 GACATTCCTCCAGACCGCAT 843
RESULT 10
B1346913 580 bp mRNA linear EST 30-JUL-2001
LOCUS B1346913
DEFINITION 376288 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION B1346913
VERSION B1346913.1 GI:15040211
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
1 (bases 1 to 580)
REFERENCE Fahrnenkung, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, B.,
Stone, R.T., Heaton, M.P., Grose, W.M., Bennett, G.A., Laegreid, W.W.,
and Keeler, J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366

Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -mismatch 12 options.

PCR Primers
 FORWARD: AGGAAACAGCTATGACCAT
 BACKWARD: GTTTCACAGTACAGCAGC
 Plate: 130 row: L column: 3
 Seq primer: ATTGATGACCTATGAC.

FEATURES
 Location/Qualifiers
 source
 1..580

/organism="Sus scrofa"
 /db_xref="taxon:9823"
 /clone_lib="MARC 2Pig"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
 library made from pooled tissue from testis, ovary,
 endometrium, hypothalamus, pituitary, and placenta."

BASE COUNT 159 a 110 c 158 g 153 t

ORIGIN

Alignment Scores:
 Pred. No.: 5.67e-87 Length: 580
 Score: 915.00 Matches: 185
 Percent Similarity: 97.44% Conservative: 5
 Best Local Similarity: 94.87% Mismatches: 3
 Query Match: 24.94% Indels: 3
 DB: 13 Gaps: 1

US-10-061-727-2 (1-687) x B1346913 (1-580)

OY 309 AepglutThrArgThGlnIleuSerIleValThSerGluAspLeuValArg 328
 Db 3 GATGAGACAGACCTCAGTCTTGGACATCAAGAACTA-CTGCTGAGATCTCAAGCCC 61
 OY 329 SerTyrValCysHisAlaArgSerIleValGluValAlaLysAlaLysValLys 348
 Db 62 AACTATGCTGTCATGCCAGAAATGCCAAGAGGAGTTCAGACCGCCGCAAGGAGAA 121
 OY 349 GlnLysValProAlaProArgTyrThrValGluLeuAlaCysGlyPheGlyAlaThrVal 368
 Db 122 CAGAAA-----GCTCCGAGATACACAGTGAAGTGGCATGTGGTTTGGAGCAGATC 175
 OY 369 LeuLeuValValIleuLeuValValIleuValIleuValIleuValIleuValIleu 388
 Db 176 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 235
 OY 389 TyrArgAlaHisPheGlyThrAspGluThrIleuAspGlyLysGlyTyrAspIleTyr 408
 Db 236 TATCGGCTCATTTTGGAAACAGATGAACATTTTGAATGGAGAAATATGATTTAT 295
 OY 409 ValSerTyrAlaArgAsnAlaGluGluGluGluPheValLeuLeuThrLeuArgGlyVal 428
 Db 236 GATCTCTATGACAGAGATCTGAGAGAGAAATTTGATTTACTACCTCCCTGGAGATC 355
 OY 429 LeuGluAsnGluPheGlyTyrIleuValCysIlePheAspArgAspSerLeuProGlyGly 448
 Db 356 TTGGAGATGATTCGAGATCAAGCTGCTCATCTTTGACCGAGACAGTGTGCTGGGAGA 415
 OY 449 AenThrValGluAlaValPheAspPheIleGlnArgSerArgArgMetIleValIleu 468
 Db 416 AATACGGTGAAGAGAGTTTGAATCTTCATTCAGAGAGCGGAGAGAGATGTGCTCG 475
 OY 469 SerProAspTyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyValMet 488
 Db 476 AGCCAGAGCTATGATGACAGAAAGAGCATCAGATCTGAGATTCAGCTGGGTGTCAAG 535
 OY 489 CysGlnAsnSerIleAlaThrLysLeuIleValGluTyrArg 503
 Db 536 TGCCAAATCTCATTCGCCAGAGCTCATTTGCTGAGTATCGT 580

RESULT 11
 AV656295 596 bp mRNA linear EST 16-JAN-2002
 LOCUS AV656295 GLC Homo sapiens cDNA clone GLCERH02.3', mRNA sequence.
 DEFINITION AV656295
 ACCESSION AV656295
 VERSION AV656295.1 GI:9877309
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 COMMENT

Contact: Zenguan Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919 (ex.45)
 Fax: 86-21-50801922
 Email: hanzg@hgc.sh.cn
 This clone is available at CHGC in Shanghai.

FEATURES
 source
 1..596
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="GLCERH02"
 /clone_lib="GLC"
 /tissue_type="corresponding non cancerous liver tissue"
 /dev_stage="Adult"
 /lab_host="SOLR"
 /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
 XhoI"

BASE COUNT 201 a 111 c 125 g 159 t

ORIGIN

Alignment Scores:
 Pred. No.: 2.39e-85 Length: 596
 Score: 900.00 Matches: 170
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.42% Mismatches: 0
 Query Match: 24.53% Indels: 0
 DB: 10 Gaps: 0

US-10-061-727-2 (1-687) x AV656295 (1-596)

OY 180 GlyCysTyrIleValIleGluAsnAsnValIleProGluGlyMetAsnLeuSerPhe 199
 Db 10 GCGCTTTAAATAATACAGAAATTTAATATATATATACCCAGATATGAACTTGAATTC 69
 OY 200 LeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValIleThrTyrProGluAsn 219
 Db 70 CTCATTTGCTTAATTTCAATTAATTAATGAAATTAACATGTTGTTACATATCCAGAAAT 129
 OY 220 GlyArgThrPheHisIleuThrArgThrLeuThrValIleValIleValIleValIleVal 239
 Db 130 GAGCTGATGTTTCATCTCAGAGACTCTGCTGTAAGAGTGAAGGCTCTCCAAAAAAT 189
 OY 240 AlaValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGly 259
 Db 190 GCAAGTCCCTCTGATATCATTCACATATGATATGATGATGATGATGATGATGATGATGAT 249
 OY 260 GluGluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGlu 279
 Db 250 GAGAGCTACTCATTCCTGATGAGCTGATTTAGTATTTCGATGAGATTCGCAATGAG 309

QY 280 ValTrrTrrThrIleAspGlyLysProAspAlaThrIleAspValThrIleAsn 299
 DB 310 GTTGGTGAACATTCATGAAAAAACCCTGATGATCATTCATTCATTCACCATTAAC 369
 QY 300 GluSerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleuSerIleLys 319
 DB 370 GAAAGATATAGTCATGATGAGACAGAGATGAAACAGAACTCAGATTTTGACATCAAG 429
 QY 320 LysValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGly 339
 DB 430 AAGTACTCTGAGAGTCTCAGCGACGACTATGCTGTCATGCTAGAGTCCAAAGGC 489
 QY 340 GluValAlaLysAlaLysValLysGlnLys 350
 DB 490 GAAATTGCCAAGCAGCCAGGTGAAACGAAA 522
 RESULT 12
 BM760155 489 bp mRNA linear EST 04-MAR-2002
 LOCUS BM760155
 DEFINITION K-EST0040658 S2SN066851 Homo sapiens cDNA clone S2SN066851-14-A03
 5' mRNA sequence.
 CCESSION
 SION BM760155 GI:19089770
 WORDS
 EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 21C Frontier Korean EST Project 2001
 Unpublished (2002)
 CONTACT Kim YS
 JOURNAL
 COMMENT
 Genome Research Institute of Bioscience & Biotechnology
 Korea Research Institute of Bioscience & Biotechnology
 52 Eosun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.krdb.re.kr
 Plate: 14 row: A column: 03
 High quality sequence stop: 489.
 FEATURES
 SOURCE
 Location/Qualifiers
 1..489
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="S2SN066851-14-A03"
 /clone_1id="S2SN066851"
 /sex="M"
 /tissue_type="Ascites"
 /cell_type="Epithelial"
 /cell_line="SNU-668"
 /lab_host="Top10F"
 /note="Organ: Stomach; Vector: pcNS; Site 1: EcoRI;
 Site 2: NotI; The poly (A)+ RNA was decapped with tobacco
 acid pyrophosphatase (TAP) and ligated with DNA-RNA linker
 including EcoRI site by treatment of T4 RNA ligase. The
 first strand cDNA was synthesized from oligo dt-selected
 mRNA by priming with dt-tailed vector. The dt-tailed
 vector was adjusted to have about 60nt. The cDNA vector
 was circularized with E. coli DNA ligase after digestion
 of EcoRI which site is also included in vector. An RNA
 strand converted to a DNA strand by Okayama-Berg method.
 The obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10F by electroporation method.
 After analyzing and sequencing about 2,000 ~ 3,000
 colonies in original cDNA library, the abundant cDNAs were
 selected and amplified by PCR reaction using vector region
 primer including T7 promoter as 5' primer and N(dT)14 as
 3' primer. The PCR products were used as template for
 synthesis of biotinylated single stranded RNA by in vitro
 transcription reaction. The synthesized RNA probes were

hybridized with antisense single stranded cDNAs prepared
 from original library and incubated with avidin-gel.
 After removing DNA-RNA hybrids by centrifuge, the
 subtracted cDNA libraries were constructed by
 transformation of the remaining DNA into competent cells E.
 coli Top10F with electroporation method."

BASE COUNT 158 a 90 c 97 g 144 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 6.07e-83 Length: 489
 Score: 876.00 Matches: 162
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 23.88% Indels: 0
 DB: 14 Gaps: 0
 US-10-061-727-2 (1-687) x BM760155 (1-489)
 QY 157 ArgIleThrCysProAsnValAspGlyTyrPheProSerSerValLysProThrIleThr 176
 DB 3 AGATCACTTGTCCAAATGATGATGATATTTCTTCAGATGCAACCACTATCACT 62
 QY 177 TrrTrrMetGlyCysTrrLysIleGlnAsnPheAsnValIleProGluGlyMetAsn 196
 DB 63 TGGTATATGGCTGTAT 122
 QY 197 LeuSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyr 216
 DB 123 TTGAGTTTCCATTCATGCGCTTATATCAATATATGAAATTCACATGATGTTTACATAT 182
 QY 217 ProGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysValAlaGlySer 236
 DB 183 CCAGAAATGAGACGTACCTTCATCTCCACGACTCGACTGTAAAGTGTAGGCTCT 242
 QY 237 ProLysAsnAlaValProProValIleHisSerProAsnAspHisValValTrrGluLys 256
 DB 243 CCNAAATATGAGATGCCCCCTGTATATCATTCACCTATATATATATATATATATATAT 302
 QY 257 GluProGluGluGluLeuLeuIleProCysThrValTrrPheSerPheLeuMetAspSer 276
 DB 303 GAACCAAGAGAGAGACTACTATTCCTGTACGGTCTATTTAGTTTCTGATGATTCCT 362
 QY 277 ArgAsnGluValTrrTrrThrIleAspGlyLysProAspAspIleThrIleAspVal 296
 DB 363 CGCAATGAGGTTTGGTGTGACCATTCATGCAAAAAACCTGATGATCATCATTCATGATCTC 422
 QY 297 ThrIleAsnGluSerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeu 316
 DB 423 ACCATTTACGAAAT 482
 QY 317 SerIle 318
 DB 483 AGCATC 488
 RESULT 13
 AA237107 598 bp mRNA linear EST 03-MAR-1997
 LOCUS AA237107
 DEFINITION mw96b02.f1 Soares mouse NML Mus musculus cDNA clone IMAGE:578507 5'
 similar to gb:X85999 M.musculus mRNA for interleukin 1 receptor
 accessory (MORUS);, mRNA sequence.
 ACCESSION AA237107
 VERSION AA237107.1 GI:1861163
 KEYWORDS
 SOURCE EST.
 ORGANISM Mus musculus.
 house mouse.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 598)
 Maier,M., Hallier,U., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Stepcoe,M., Tan,F., Underwood,K., Moore,B.,
 Meising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

Oy	220	GlyAsg-ThrPheHisIleThrArgThrLeuTrValLysValValGlySerProLysAs	239
Db	168	GGAGCTGACGTTCATCTCCACCGAGACTGCAGTGAAGGTAAGTAGGCTTCCTCAAAAA	227
Oy	239	nAlaValProProValIleHisSerProAsnAspHisValValIyrGILylSGluProGI	259
Db	228	TCCAGTGCCCCCGTGGATCATTCACCTATATATATCATGTGGTTATGAGAAGAACCAAG	287
Oy	255	yGlutIleLeuLeuIleProCysThrValIyrPheSerPheLeuMetAspSerArgAsnGI	279
Db	288	ACAGGAGCTACATCATTCCTCGTACCGCTCATTTTAACTTTCATGATGATTCTCCAAATGA	347
Oy	279	vAlaITPrTPTrIIleAspSGlYlysSerProAspAspIlethrIIleAspValThrlIleS	299
Db	348	GGTTTGTTGGACCATTGATGAGAAAATAAACCTGATGTCATCATCATTAAGATGACCAATTAA	407
Oy	299	nGluSerIleSerHisSerArgThrGluAspGluThrArgTrnGlnIleLeuSerIleLy	319
Db	408	CGAAGTATTAAGTCATATGTAAGAACAGAAATGAAACAAACAATCTCAGATTMTAGCATCAA	467
Oy	319	sIysValIthrSerGluAspLeuLysArgSerTyValCyshIsalArgSerAlaLysGI	339
Db	468	GAAAGTACTCTCTGAGGATCTCAAGCGCAGCATATGCTCTCATGTCAAGAAGGCCANNNG	527
Oy	339	yGluValAlaLysAlaLysValLysGlnLys	350
Db	528	CGAAGTTGCCAAGACGCCAAGGTGAAGCAGAAA	561
RESULT 15			
LOCUS	B6625831	652 bp mRNA linear EST 31-AUG-2001	
DEFINITION	B6625831 RIKEN full-length enriched, adult male diencephalon Mus		
ACCESSION	B6625831		
VERSION	B6625831.1 GI:15398624		
KEYWORDS	EEST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Kushiyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
	1 (bases 1 to 652)		
	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanaagaki,T., Hara,A.,		
	Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawat,J., Komno,H., Kouda,		
	'M., Koya,S., Matsuyama,T., Miyazaki,I., Nomura,K., Ohno,M.,		
	Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,		
	'D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,		
	Tagami,M., Tagawa,A., Takahashi,P., Takeda,Y., Tanaka,T., Toya,T.,		
	Muramatsu,M. and Hayashizaki,Y.		
	RIKEN Mouse ESTs (Arakawa,T., et al. 2001)		
	Unpublished (2001)		
TITLE	Contact: Yoshihide Hayashizaki		
JOURNAL	Laboratory for Genome Exploration Research Group, RIKEN Genomic		
	Sciences Center(GSC), Yokohama Institute		
	The Institute of Physical and Chemical Research (RIKEN)		
	1-7-22 Suhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan		
	Tel.: 81-45-503-9222		
	Fax: 81-45-503-9216		
	Email: genome-res@gs.c.riken.go.jp,		
	URL:http://genome.gsc.riken.go.jp/		
	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh		
	'M., Komno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.		
	Normalization and subtraction of cap-trapper-selected cDNAs to		
	prepare full-length cDNA libraries for rapid discovery of new		
	genes. Genome Res. 10 (10), 1617-1630 (2000)		
	wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,		
	Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunura		
	'S., Kawat,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and		
	Hayashizaki,Y.		
	RIKEN integrated sequence analysis (RISA) system--384-format		
	sequencing pipeline with 384 multicapillary sequencer. Genome Res.		
	10 (11), 1757-1771 (2000)		
	Komno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara		
	'Y. and Hayashizaki,Y.		

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)

Yamada, I., Kiyosawa, H., Kondo, S., Saito, T., Shingawa, A., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arkawa, T., Ishii, Y. and Hayashizaki, Y.

Mapping of 19032 mouse cDNAs on mouse chromosomes. *J. Struct. Funct. Genomics* 2 pre, 172-186 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

mouse tissues.

	BASE COUNT	153 a	171 c	168 g	159 t	1 others
ORIGIN						
Alignment Scores:						
Pred. No.:		8.7e-81		Length:		652
Score:		858.00		Matches:		155
Percent Similarity:		94.22%		Conservative:		8
Best Local Similarity:		89.60%		Mismatches:		10
Query Match:		23.39%		Indels:		0
DB:		10		Gaps:		0
US-10-061-727-2 (1-687) x BB625831 (1-652)						
OY	1	MecThrieuLeuTpyCySValSerLeuTyRPheryrGlyIleuGInSerAspa	20			
Db	133	ATGGAGCTTCCTGCGGTATTGATGAGCTCTGCTTCATATGGAGATCCGCGAGATCAAGCT	192			
OY	21	SerGIuArGcYsaSPaPTpGILyLeuAspThrMerArgInIleGInValPheGluAsp	40			
Db	193	TGGAGCGCTGTGATGATGACTGGGAGCTGATGATCCATGCGACAAATCCAGTCTTTGAGAT	252			
OY	41	GIuProIaArGIlelyCySPoleuPheGluHisPheLeuIySPheAsuTySerThr	60			
Db	253	GAGCGCGCTCGAATCAAGTCCCCCTCTTGAACAATCTCCGAAGTCAACTACAGCACT	312			
OY	61	AlaHisSerIaGIyLeuThrLeuIleTpyTyTTrpThArGIuAspAgaSPLeuGIu	80			
Db	313	GCCCATTCCTCTGGCTTACCTCGATCTGTATCTGACACAGCGAAGCCGGAGACTGGAG	372			
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 job time : 1684 secs

GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 30, 2003, 06:44:49 ; Search time 3717 Seconds

(without alignments)
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Total number of hits satisfying chosen parameters: 4109280

Minimum DB seg length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1388.4	67.3	1740	9	AF029213
3	1388.4	67.3	4724	9	AB006537
4	1067.4	51.7	3355	6	ARI66116
5	1067.4	51.7	3355	10	MM1LRACP
6	1051	50.9	1857	9	AF167343
7	1049.8	50.9	1862	10	RNT48592
8	793.4	38.4	1916	10	BC021159
9	776.4	37.6	2226	9	AK095107
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11	515	25.0	58987	2	AC119283
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18	153.8	7.5	2102	9	FI6733S09
19	151	7.3	2061	6	ARI79668
20	151	7.3	2061	9	AF212016
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ACCESSION ARI66115
VERSION ARI66115.1 GI:16241289
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1740)
AUTHORS Cao, Z.
TITLE Interleukin-1 receptor accessory proteins, nucleic acids and
methods
JOURNAL Patent: US 6280955-A 1 28-AUG-2001;
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 Best Local Similarity 89.6%; Pred. No. 0;
 Matches 1517; Conservative 0; Mismatches 171; Indels 6; Gaps 2;

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 VERSION AF029213.1 GI:2599126
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 1740)
 AUTHORS Huang, J., Gao, X., Li, S. and Cao, Z.
 TITLE Recruitment of IRAK to the interleukin 1 receptor complex requires
 interleukin 1 receptor accessory protein
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (24), 12829-12832 (1997)
 MEDLINE 98058729
 PUBMED 9371760
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AUTHORS Huang, J., Gao, X., Li, S. and Cao, Z.
TITLE Direct Submission
JOURNAL Submitted (07-Oct-1997) Biology, Tularik, Inc., 2 Corporate Dr.,
South San Francisco, CA 94080, USA

FEATURES Location/Qualifiers

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Best Local Similarity 89.6%; Pred. No. 0;

Matches 1517; Conservative 0; Mismatches 171; Indels 6; Gaps 2;

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TITLE	Interleukin-1 receptor accessory proteins, nucleic acids and methods
JOURNAL	Patent: US 6280955-A 3 28-MUG-2001;
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Best Local Similarity	78.9%; Pred. No. 2.3e-296;
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Oy	841	TGTGTGACCAATGTATGAGAAAAAAACCTGATGACATCACTATTTGATGTCAACCTTAAAGAA	900
Db	975	TGTGTGACCAATTTATGAGAAAAAGCCTGTATGACGTCACTGACATCACTATTTATATATAA	1034
Oy	901	AGTATAGTCAATAGTATGAAACAGAAAGATGAAACAGAACTCAGATTTTGAGATCAAGAAA	960
Db	1035	AGTATAGTATTTCTTCAACGAAAGATGAAACAGAACTCAGATTTTGAGATCAAGAAA	1094
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Db	1095	GTCAACCCCGAGGATCTCAGGGCGCACTATGTCTGTATGCTGAAATATACAAAGCGAA	1154
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Db	1155	GCTAGACAGGCTCGCAAGGTGAAGCAAGAAAGTCAACCAACCAAGGTATACAGATGAACTTC	1214
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Db	1215	GCTGTGTGTTTGAAGCAAGGCTTTCGTAAGTGTGTTCTCATGTGTGTTTACCATGTT	1274
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Db	1275	TACTGCTAGATATGTCCTCTTTTACGAGCTCACTTTTGAAACAGATGAACAATTTCTT	1334
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Oy	1261	GTATTAATGACCTCGGTGAGATTTTGGAGATGAAATTTGATACAACTGTGCAATCTTT	1320
Db	1395	GTCGTGCTGACGCTCGGTGAGATTTTGGAGATGAAATTTGATACAACTGTGCAATCTTT	1454
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Db	1455	GACCGAACAAGCTCTGCGGGAAATATGCAAGATGAAACCTGTAGCTTCAATTCAGAA	1514
Oy	1381	AGCAAGAGATGATGTGTTCTGACCCCTGATATGTGACAAAAAGACATCAGATG	1440

QY	661	CGTACGTTTCATCTACACCGAGACTGCTGATGAAAGTGTAGGCTCTCCAAATAATGCA	720
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QY	721	GTGCCCCCTGTATCCATTCACTTAATGATCATGTGCTTATGAGAAAGACACGAGAG	780
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QY	781	GAGCTACTCATTCCTCTGTAACGCTTATTTTACTTTTCTGATGGAATTTCTGCAATGAGTT	840
Db	781	GAGCTACTCATTCCTCTGTAACGCTTATTTTACTTTTCTGATGGAATTTCTGCAATGAGTT	840
QY	841	TGCTGACCATTTGATGAGAAAAAAACCCTGATGACATCATTAATGATGTCCATTAAACGA	900
Db	841	TGCTGACCATTTGATGAGAAAAAAACCCTGATGACATCATTAATGATGTCCATTAAACGA	900
QY	901	AGTATTAAGTCATAGTAGAACAAGAGATGAAACAGAACTCAGATTTTGGATCAAGAAA	960
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QY	961	GTTACCTCTGAGAGATCTCAAGCGCAGCTATGTCTGTCTAGTAGAAGTCCAAAGCGAA	1020
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DEFINITION	Rattus norvegicus interleukin-1 receptor accessory protein (IL-1)		
ACCESSION	U48592		
VERSION	U48592.1	GI:1403699	
KEYWORDS			
ORGANISM	Rattus norvegicus.		
SOURCE	Rattus norvegicus.		
REFERENCE	1 (bases 1 to 1862)		
AUTHORS	Liu, C., Chalmers, D., Maki, R. and De Souza, E.B.		
TITLE	Rat homolog of mouse interleukin-1 receptor accessory protein: cloning, localization and modulation studies		
JOURNAL	J. Neuroimmunol. 66 (1-2), 41-48 (1996)		
PUBMED	89626535		
REFERENCE	2 (bases 1 to 1862)		
AUTHORS	Liu, C.		
TITLE	Direct Submission		
JOURNAL	Submitted (06-FEB-1996) Changlin Liu, Molecular Biology, Neuroocrine		
FEATURES	Biosciences, Inc., 3050 Science Park RD, San Diego, CA 92121, USA		
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	NORLHLRTMTVTKVYGSKPAKVAPEHYISPNDRVYKREDEELVYPKKYFSPFMS		
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Db	163	TCCGAACGCTCTGATGATGACTGGGGACTGATATCCATGCGACAAATCCAAAGTCTTGAAGAT	222
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Db	703	ATCCCCCTTGATTAATAATACGAATATTAACATGTGTGTGATGATATCTGGAAGAAACGGA	762
OY	661	CGTACGTTCACTTCCACGAGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA	720
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OY	781	GAGGACTCATTTCCCGTAGSGTCTAATTATGTTTCTTGAAGGATTTCCGCAATGAGGTT	840
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OY	841	TGTGAGACCATTTGATGGAAGAAAGAAACCTGATGACATCACTATATGATGTCAACCATTAACGAA	900
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 Db 613 CCAATATGATGATGATATTTTCTTCCAGTGTCAAAACCGATCATCTGGTATATGGGT 672
 Oy 541 TGTATTAATATGATATTTTATATATATATATATATATATATATATATATATATAT 600
 Db 673 TGAATGAAATATGATGATATTTTATATATATATATATATATATATATATATATAT 732
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 Oy 661 CCGATGTTTCAAT 720
 Db 793 CCGTCTTGTGTTTCAAT 852
 Oy 721 GTGCCCCCTGAT 780
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 Oy 781 GAGTACATCATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
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RESULT 9
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 ACCESSION AK095107
 VERSION AK095107.1 GI:21754300
 SOURCE Homo sapiens; tissue: testis; library: BRL; clone: BRHIP2028593.
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 Nishimura, K., Magatsuma, M., Kanda, K., Kondo, H., Yokoi, T., Kodaira, H., Furuya, T., Takahashi, M., Kikkawa, B., Omura, Y., Abe, K., Kamihara, K., Katsura, N., Sato, K., Tanikawa, M., Yamazaki, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai, H., Matsuo, K., Nakamura, Y., Sekine, M., Kimura, K., Yamashita, H., Matsuo, K., Kaneko, K., Takahashi, F., Fujii, A., Okuchi, H., Murakawa, K., Kanehori, K., Takahashi, F., Sugino, S., Ohnishi, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Nagai, K., and Isogai, T.
 Nagai, K., Masuho, Y., Nagai, K., and Isogai, T.
 NEDO human cDNA sequencing project
 TITLE Unpublished
 JOURNAL 2 (bases 1 to 2226)
 REFERENCE Isogai, T. and Yamamoto, J.
 AUTHORS Direct Submission
 JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

COMMENT
 (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
 NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

FEATURES
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BASE COUNT 629 a 480 c 509 g 608 t

Query Match 37.6%; Score 776.4; DB 9; Length 2226;
 Best Local Similarity 99.7%; Pred. No. 2.1e-212;
 Matches 777; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Dn	601	CAGAGATTTCATACCAAGCCCCAGTGGGAGACACACCTCTGTAGCCTGTTCC	CAAGAGT	660
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VERSION	BAC Library) complete sequence.			
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SOURCE	HTG.			
ORGANISM	human.			
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AUTHORS	Euhariyotia; Euteleostomi; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 46509) Muzny D.M., Adams C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Albrooks, S.L., Amaralunge, H.C., Are, J.R., Ayale, M., Banks, T., Bardetta, J., Benton, J., Blumage, K., Blumenthal, K., Bonin, N.P., Book, A.J., Bowls, S., Brileva, M., Brown, E., Brown, M., Bryant, N.P., Bunyah, C., Butch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carroll, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhury, I., Christopoulos, S., Clelland, C.D., Cox, C., Coyle, M.D., Datborne, S.R., David, R., Dayila, M.L., Davis, C., Davy-Garroll, L., Dedrich, D.A., DeLanay, K.R., Delgado, O., Dem, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gotelli, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlik, P., Hawes, A., He, X., Hernandez, J., Hernandez, O., Hodgson, A., Hughes, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulys, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivert, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratochvic, J., Kuresh, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, K.J., Liu, W., Lousheed, H., Lozano, R., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapa, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mashiney, E., McLeod, M.P., Meador, M., Mel, G., Metzger, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Moore, S., Morgan, M., Moorish, T., Morris, S., Moser, M., Neel, D., Neelson, D., Newton, J., Newsum, N., Nguyen, A., Nguyen, N., Nguyen, N., Nixonson, E., Nwokkenko, S., Ogih, M., Okunoye, G., Oraduy, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Prims, E., Pu, L.L., Quiles, M., Ren, Y., River, M., Rojas, A., Roubockan, I., Rolfe, R., Ruiz, S., Savory, G., Scherer, S., Scott, G., Shen, H., Shoshitari, N., Sisom, I., Sodergren, E., Sonalkhe, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabori, P., Tametria, A., Tametria, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, R., Thomas, S., Usmani, K., Vazquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Naylor, S.L., Weinstein, G. and Gibbs, R.			
TITLE	Direct Submission			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 46509)			
AUTHORS	Worley, K.C.			

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TITLE      Direct Submission
JOURNAL    Submitted (31-JAN-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3 (bases 1 to 46509)
AUTHORS     Morley,K.C.
TITLE      Direct Submission
JOURNAL     Submitted (03-JUN-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   4 (bases 1 to 46509)
AUTHORS     Morley,K.C.
TITLE      Direct Submission
JOURNAL     Submitted (21-JUN-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Jun 21, 2002 this sequence version replaced gi:21306532.
            INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
            gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the
entire insert of this clone. Overlapping regions of clones are only
sequenced and submitted once, so the sequence for the remainder of
the insert may be found in the record for the adjacent clones.
Overlapping clones are noted at the beginning and end of the
Features listing.

ANNOTATION OF FEATURES:
STS are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green,
unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST
(Nuc. Acids Res. 25:3389-3402), similarity (expect < 1e-34) to the
EST and cDNA sequences. Genes demonstrate at least two exons
flanked by consensus splice sites that maintained sequence
continuity across the splice junctions. Sequences that are not
identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
standard of double strand coverage with a minimum of 2 clones and 2
reads with no ambiguities or 2 chemistries with a minimum of 2
clones and 3 reads with no ambiguities. If the sequence quality for
a region does not meet this standard, it will be indicated in the
annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
standards - estimated error rate less than 1 per 10,000 bases.
Reports of lowest quality individual bases and measures of base
quality are listed below. Description of the metrics can be found
at URL: http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annot
action.html.

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/rpt_family="(TG)n"
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/rpt_family="MER31B"
repeat_region 24689..24727
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repeat_region 24728..25024
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STS 25377..25763
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STS 26576..26677
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repeat_region 26649..26742
/rpt_family="MIR"
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/rpt_family="AT_rich"
repeat_region complement(27489..27606)
/rpt_family="MER5A"
repeat_region 27758..27935
/rpt_family="MER5A"
repeat_region complement(28183..28293)
/rpt_family="MLT11"

Query Match 34.8% Score 718.4; DB 9; length 46509;

Best Local Similarity 99.7%; Pred. No. 1.7e-195;
Matches 719; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1344 AATATAGTGAAGAGATTTTGAATTCATTCAGAGAGAGAGATGTTTCT 1403
| | | | |
DB 22840 AGATACAGTGAAGAGATTTTGAATTCATTCAGAGAGAGATGTTTCT 22899
| | | | |
QY 1404 GAGCCCTGATATGTCAGAGAGAGAGATGTCAGAGATGTTTCT 1463
| | | | |
DB 22900 GAGCCCTGATATGTCAGAGAGAGAGATGTCAGAGATGTTTCT 22959
| | | | |
QY 1464 GTCAGAGATTCATTCAGAGAGAGAGATGTCAGAGATTCATTCAGAGATTC 1523
| | | | |
DB 22960 GTCAGAGATTCATTCAGAGAGAGAGATGTCAGAGATTCATTCAGAGATTC 23019
| | | | |
QY 1524 GCACCCAGGATTCATTCAGAGAGAGAGATGTCAGAGATTCATTCAGAGATTC 1583
| | | | |
DB 23020 GCACCCAGGATTCATTCAGAGAGAGAGATGTCAGAGATTCATTCAGAGATTC 23079
| | | | |
QY 1584 GTCCAAATTCATTCAGAGAGAGAGATGTCAGAGATTCATTCAGAGATTC 1643
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QY 1644 TCTGATGTCAGATTCATTCAGAGAGAGAGATGTCAGAGATTCATTCAGAGATTC 1703
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| | | | |
QY 1704 TCACGTTCAAGAGAGAGAGAGAGAGATGTCAGAGATTCATTCAGAGATTC 1763
| | | | |
DB 23200 TCACGTTCAAGAGAGAGAGAGAGAGATGTCAGAGATTCATTCAGAGATTC 23259
| | | | |
QY 1764 GCTCAGATGAGCTTCAGAGAGAGAGATGTCAGAGATTCATTCAGAGATTC 1823
| | | | |
DB 23260 GCTCAGATGAGCTTCAGAGAGAGAGATGTCAGAGATTCATTCAGAGATTC 23319
| | | | |
QY 1824 CACCTGCGGATGTCAGAGAGAGAGATGTCAGAGATTCATTCAGAGATTC 1883
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DB 23380 GGCAGAGATTCATTCAGAGAGAGAGATGTCAGAGATTCATTCAGAGATTC 23439
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QY 1944 GTGAGAACTGATGATTCAGAGAGAGATGTCAGAGATTCATTCAGAGATTC 2003
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DB 23440 GTGAGAACTGATGATTCAGAGAGAGATGTCAGAGATTCATTCAGAGATTC 23499
| | | | |
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DB 23500 AGCCCTGCTTCATTCAGAGAGAGATGTCAGAGATTCATTCAGAGATTC 23559
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QY 2064 A 2064
DB 23560 A 23560

RESULT 11
AC119283/c 58987 bp DNA linear HTG 25-APR-2002
LOCUS AC119283
DEFINITION Mus musculus clone RP24-345H5, LOW-PASS SEQUENCE SAMPLING.
AC119283
ACCESSION AC119283
VERSION AC119283.1 GI:20304009
KEYWORDS HTG; HTGS PHASE0.
SOURCE Mus musculus.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 58987)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Mus musculus, clone RP24-345H5
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 58987)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,

TITLE
JOURNAL
COMMENT

Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,
Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., Deatrellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R.,
Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G.,
McClerny, C., Macdonald, P., Major, J., Margulis, N., Matthews, C.,
McCarthy, M., McSwan, P., McKernan, K., Meldrum, J., Menes, L.,
Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,
Olivier, J., Peterson, K., Punthang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R.,
Seaman, S., Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N.,
Straus, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (25-APR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Salt, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: L25964

Center clone name: 345_H_5

* NOTE: This record contains 72 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

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Query Match 25.0%; Score 515; DB 2; Length 58987;
Best Local Similarity 86.4%; Pred. No. 8.7e-117;
Matches 603; Conservative 0; Mismatches 88; Indels 7; Gaps 3;

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Db 7231 GTAGATACCGTGAAGAGCTTTTGTATTCATTCAGAGAGAGAGATGATGTTT 7272

Qy 1402 CTGAGCCCTGCTATGTGACAGAAAGAGATCGAGATGCTGAGTTTAACTGGGTGTC 1461
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Db 7271 CTGAGCCCTGCTATGTGACAGAAAGAGATCGAGATGCTGAGTTTAACTGGGTGTC 7212

Qy 1462 ATGTGCGAGAACTTCATTCAGAGATGCTGATGTTGATGATCCCTTCAGAC 1521
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Db 6914 GAGGAGCTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6855
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Qy 1881 CCGGAGAGAGATTCATTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1940
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Db 6677 CTCAGCTTCCTGCACTCCGCACTTTCAGAGAGATTCGA 6640

RESULT 12
F167333504 890 bp DNA linear PRI 24-MAY-2000
LOCUS Homo sapiens interleukin 1 receptor accessory protein (IL1RAP)
DEFINITION gene, exon 4.
ACCESSION AF167336
VERSION AF167336.1 GI:8050492
KEYWORDS 4 of 10
SEGMENT Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 890)
AUTHORS Jensen, L.E., Wuzio, M., Mantovani, A. and Whitehead, A.S.
TITLE IL-1 signaling cascade in liver cells and the involvement of a
soluble form of the IL-1 receptor accessory protein.
JOURNAL J. Immunol. 164 (10), 5277-5286 (2000)
MEDLINE 20261666
PUBMED 10793889
REFERENCE 2 (bases 1 to 890)
AUTHORS Jensen, L.E.
TITLE Direct Submission
JOURNAL Submitted (09-JUN-1999) Department of Pharmacology, University of
Pennsylvania, 156 Johnson Pavilion, 3620 Hamilton Walk,
Philadelphia, PA 19104, USA
FEATURES
source 1..890
location/Qualifiers
exon /db_xref="taxon:9606"
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BASE COUNT 240 a 192 c 186 g 272 t
ORIGIN
Query Match 14.2%; Score 292.8; DB 9; Length 890;
Best Local Similarity 97.7%; Pred. No. 6.9e-73;
Matches 297; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db	714	AGCCATTACTTCGGCTCCCGGAGAACCGATTAGTAGAGAAATGTCGTGCT	773
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Db	774	TCGGGCGCACTCTCTCAATGACACTGGCAACTATACCTGCATGTTAAGTAGCTAAT	833
Qy	362	ATTG 365	
Db	834	CTTG 837	
RESULT 13			
AC008249		184203 bp	DNA linear PRI 21-JUN-2002
LOCUS			
DEFINITION			Homo sapiens 3 BAC RP11-211P13 [Roswell Park Cancer Institute Human
SESSION			BAC Library] complete sequence.
AC008249			
AC008249.14		GI:6137875	
HTG.			
KEYWORDS			
ORGANISM			human.
REFERENCE			
AUTHORS			Homo sapiens
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
			Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
			1 (bases 1 to 184203)
			Muzny,D.M., Adams,C., Bailey,M., Barbara,J., Blankenburg,K.,
			Bodot,B., Bouck,J., Bowie,S., Brooks,A., Buhey,C., Bunac,C.,
			Burkett,C., Burrows,J., Carter,M., Chacko,J., Chen,Z., Cox,C.,
			David,R., Delgado,O., Deshazo,D., Ding,Y., Donah-Rashid,N.,
			Dugan-Rocha,S., Durbin,K.J., Fernandez,C., Ferraguto,D.,
			Forcum-Tansey,J., Frantz,P., Ganesh,R., Garcia,D.K., Gorell,J.H.,
			Gorell,L.L., Guevara,W., Harris,K., He,X., Hernandez,J.,
			Hodgson,A., Hognes,M., Holloway,C., Hosak,H., Jackson,L.E.,
			Jackson,L., Jia,Y., Jones,M., Kelly,S., Kondesewski,N., Kong,Y.,
			Kovar,C., Leal,B., Li,Z., Lichtarge,O., Liu,J., Liu,W., Logan,O.,
			Lu,J., Lucier,R., Martin,R., Martinez,C., McLeod,M.P., Mei,G.,
			Moore,S., Moorish,T., Morgan,M., Morris,S., Nash,S., Nelson,A.,
			Nguyen,R., Nguyen,N., Nguyen,S., Oswal,G., Parish,B., Paxton,S.,
			Payton,B., Perez,L., Pu,L.L., Quiles,M., Reiter,D., Rives,M.,
			Samuel,S., Say,J., Scherer,S., Shah,E., Shen,H., Simon,M.,
			Sparks,A., Stamps,A., Sugang,R., Taber,P., Taylor,T., Vasquez,L.,
			Vinson,R., Vo,O., Wahbah,M., Watlington,S., Weinstein,G.,
			Weinstock,I.R., Williamson,A., Worley,K., Wren,J., Wrenford,G.,
			Yu,W., Zhou,X., Naylor,S.L., Nelson,D. and Gibbs,R.
			Direct Submission
			2 (bases 1 to 184203)
			Worley,K.C.
			Direct Submission
			Submitted (30-JUL-1999) Human Genome Sequencing Center, Department
			of Molecular and Human Genetics, Baylor College of Medicine, One
			Baylor Plaza, Houston, TX 77030, USA
			3 (bases 1 to 184203)
			Worley,K.C.
			Direct Submission
			Submitted (20-OCT-1999) Human Genome Sequencing Center, Department
			of Molecular and Human Genetics, Baylor College of Medicine, One
			Baylor Plaza, Houston, TX 77030, USA
			4 (bases 1 to 184203)
			Worley,K.C.
			Direct Submission
			Submitted (15-MAY-2002) Human Genome Sequencing Center, Department
			of Molecular and Human Genetics, Baylor College of Medicine, One
			Baylor Plaza, Houston, TX 77030, USA
			5 (bases 1 to 184203)
			Worley,K.C.
			Direct Submission
			Submitted (21-JUN-2002) Human Genome Sequencing Center, Department
			of Molecular and Human Genetics, Baylor College of Medicine, One
			Baylor Plaza, Houston, TX 77030, USA
			On Oct 28, 1999 this sequence version replaced gi:6091634.
			INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
			gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect $< 1e-34$) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT-----

Summary Statistics	
Contig length:	184203
Phrap values in estimate:	183529
Average error rate (RCM-phrap estimate):	1.29501e-05
Fraction of Phrap values less than 40 :	0.0125648
Number of consensus changing edits:	0
Number of N's in consensus :	0

Position	Consensus	changing edits	Edited-Context
6949	aaggagctg (n)	acaactcttt	aaggagctg (c)
14835	tctatattg (t)	tttatctctc	ctctatattg (t)
17123	gaggaagaag (n)	caactgcact	gaggaagaag (a)
17130	taaggacgag (n)	agcaattagg	taaggacgag (a)

----- Distribution of Quality < 40 Bases -----

# bases	Phrap Value Range
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900	35-40
800	35-40
700	35-40
600	35-40
500	35-40
400	35-40
300	35-40
200	35-40
100	35-40
0	5-10

1. .184203

Oy	62	CAGAACGCTGGGAATCACTGGGGACCTAGCACACCATGAGGCAAATCCAGTGTTCAGAATG	121
Db	153275	CAGAACGCTGGGAATCACTGGGGACCTAGCACACCATGAGGCAAATCCAGTGTTCAGAATG	153334
Oy	122	AGCAGACTCGCATCAAGTGCCCACTTTTGAACAATTCTTGAATCACTACAGCAACG	181
Db	153335	AGCAGACTCGCATCAAGTGCCCACTTTTGAACAATTCTTGAATCACTACAGCAACG	153394
Oy	182	CCCATTCAGCTGGGCTTAATCTGTGATTTGTGTATTTGGAATAAGGACGACCGGACCTTGGG	241
Db	153395	CCCATTCAGCTGGGCTTAATCTGTGATTTGTGTATTTGGAATAAGGACGACCGGACCTTGGG	153454
Oy	242	AGCCAATTAATCTTCGCCCTCCCCGAGAACCGCATTTAGTAAGAGAAAAGATGTGCTGTGT	301
Db	153455	AGCCAATTAATCTTCGCCCTCCCCGAGAACCGCATTTAGTAAGAGAAAAGATGTGCTGTGT	153514
Oy	302	TCCGGCCCACTCTCTCTCAATGACACTGGCAACTAATACCCTGCATGTTAAGAACTACAT	361
Db	153515	TCCGGCCCACTCTCTCTCAATGACACTGGCAACTAATACCCTGCATGTTAAGAGCTGATY	153574
Oy	362	ATTG 365	
Db	153575	CTTG 153578	
RESULT 14			
AC098400/c		87015 bp	DNA linear HTG 31-JUL-2002
LOCUS		Rattus norvegicus clone CH230-2B16,	*** SEQUENCING IN PROGRESS ***
DEFINITION		49 unordered pieces.	
ACCESSION		AC098400	
VERSION		AC098400.2 GI:21953618	
KEYWORDS		HTG; HTGS; PHASEI.	
SOURCE		Norway rat.	
ORGANISM		Rattus norvegicus	
		Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;	
		Rattus.	
REFERENCE		1 (bases 1 to 87015)	
AUTHORS		Wuzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaralunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimoge,K., Blankenburg,K., Bonnin,D., Bouch,R.J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buahy,C., Burck,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carroll,T.F., Carter,M., Cavazos,S.R., Checko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dedertich,D.A., Delaney,K.R., Delgado,O., Dem,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferriguto,D., Flaeggen,N., Ford,J., Foster,P., Franz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorelli,J.H., Guevara,M., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlik,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hognes,M., Holloway,C., Hollins,B.E., Homsi,P., Howard,S., Huber,V., Huylk,S., Hume,J., Jackson,L.B., Jacobson,B., Jia,Y., Johnson,R., Jolyvet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Koryah,J., Kovari,C., Kratochvic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichteage,O., Lieu,C., Liu,J., Liu,W., Loulesged,H., Lozado,R.J., Lu,X., Lucier,A., Lucieri,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M., Miner,G., Minner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newsum,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,B., Nwokwenkwos,S., Oguh,M., Okunodu,G., Orangunye,N., Oyedero,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Preece,E., Pullin,L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojudoakan,I., Rolfe,M., Ruiz,S., Savery,G., Shaner,S., Scott,G., Shen,H., Shoshchari,N., Stason,I., Soderstrom,E., Sonaik,T., Sparks,A., Stanley,H., Stone,H.,	

Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wallington, S.,
Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G., and Gibbs, R.

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLES
JOURNALS

Unpublished
2 (bases 1 to 87015)
Morley, K. C.
Direct Submission
Submitted (23-OCT-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 87015)
Morley, K. C.
Direct Submission
Submitted (31-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 24, 2002 this sequence version replaced gi:16328167.

Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: TUPS
Center clone name: CH230-2B16
Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 45081 bases at least Q40
Consensus quality: 48248 bases at least Q30
Consensus quality: 50450 bases at least Q20

NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
* consists of 49 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1158: contig of 1158 bp in length
1 1159 1258: gap of unknown length
1 1259 2609: contig of 1351 bp in length
2610 2709: gap of unknown length
2710 3789: contig of 1080 bp in length
3790 3889: gap of unknown length
3890 5261: contig of 1372 bp in length
5262 5361: gap of unknown length
5362 6887: contig of 1526 bp in length
6888 6987: gap of unknown length
6988 8178: contig of 1191 bp in length
8179 8278: gap of unknown length
8279 10098: contig of 1820 bp in length
10099 10198: gap of unknown length
10199 11473: contig of 1275 bp in length
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11574 12857: contig of 1284 bp in length
12858 12957: gap of unknown length
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16793 18265: contig of 1473 bp in length
18266 18365: gap of unknown length

18366 19474: contig of 1109 bp in length
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20596 20695: gap of unknown length
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21998 23684: contig of 1687 bp in length
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35319 37253: contig of 1936 bp in length
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37354 39619: contig of 2266 bp in length
39620 39719: gap of unknown length
39720 40790: contig of 1071 bp in length
40791 40890: gap of unknown length
40891 42193: contig of 1303 bp in length
42194 42293: gap of unknown length
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43367 43466: gap of unknown length
43467 45401: contig of 1935 bp in length
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45502 47554: contig of 2053 bp in length
47555 47655: gap of unknown length
47656 50095: contig of 2441 bp in length
50096 50195: gap of unknown length
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52026 54851: contig of 2827 bp in length
54852 54951: gap of unknown length
54952 55965: contig of 1014 bp in length
55966 56065: gap of unknown length
56066 57562: contig of 1497 bp in length
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63230 63329: gap of unknown length
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72162 74907: contig of 2746 bp in length
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77634 79956: contig of 2323 bp in length
79957 80056: gap of unknown length
80057 83710: contig of 3654 bp in length
83711 83810: gap of unknown length
83811 87015: contig of 3205 bp in length.

FEATURES
source
1. .87015
Location/Qualifiers

GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 30, 2003, 06:43:29 ; Search time 320 Seconds

(without alignments)
14525.389 Million cell updates/sec

Title: US-10-061-727-1

Perfect score: 2064

Sequence: 1 atgacactctctgctgtgtc.....acgactttatctcctataa 2064

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
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23: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1388.4	67.3	1740	23 AAS15608 Human interleukin-1
2	1385.2	67.1	1713	17 AAT32026 Human interleukin-1
3	1075.4	52.1	1077	17 AAT32027 Soluble interleukin-1
4	1069.2	51.8	2733	21 AAO9048 Fusion polypeptide
5	1067.4	51.7	1713	17 AAT32028 Mouse interleukin-1
6	1067.4	51.7	3355	23 AAS15609 Mouse interleukin-1
7	1047.8	50.8	2155	19 AAV3659 Human interleukin-1
8	287	13.9	287	22 AAI24540 Probe #14473 for g
9	287	13.9	287	22 AAI49786 Probe #18472 used

10	220	10.7	478	22 AAI15283	Probe #5216 for ge
11	220	10.7	478	22 AAI36611	Probe #5297 used t
12	164.2	8.0	246	24 ABN18246	Human ORFX polynuc
13	151	7.3	2061	20 AAS58245	Human IL-1Rd codi
14	151	7.3	2061	24 AAD27170	Human interleukin-
15	149	7.2	169	22 ABA50826	Human breast cell
16	149	7.2	169	22 ABA68793	Human foetal liver
17	149	7.2	169	22 ABA35757	Probe #14223 for g
18	149	7.2	169	22 AAI17135	Human brain expres
19	149	7.2	169	22 AAK42922	Human bone marrow
20	149	7.2	169	22 AAI23682	Probe #13615 for g
21	149	7.2	169	22 AAI48995	Probe #17681 used
22	149	7.2	169	22 AAI09300	Probe #9291 used t
23	149	7.2	169	24 ABA16980	Human genome-deriv
24	146	7.1	1979	20 AAX84308	Human TIGIR codin
25	145.2	7.0	2091	21 AAI27919	Human Xrec2 cDNA c
26	145.2	7.0	3122	22 AAK51941	Human polynucleoti
27	144.4	7.0	2537	24 AAD27179	Human interleukin-
28	142	6.9	3120	22 ABA09029	Human oligophrenin
29	142	6.9	3120	22 AAK52925	Human polynucleoti
30	139.4	6.8	1737	20 AAK58247	Human IL-1Rd codi
31	139.4	6.8	1737	24 AAD27169	Human interleukin-
32	113.6	5.5	443	24 ABA97121	Gene #3619 used to
33	96	4.7	229	21 AAC09103	Human secreted pro
34	95	4.6	400	22 ABA45706	Human breast cell
35	95	4.6	400	22 ABA56209	Human foetal liver
36	95	4.6	400	22 ABA25860	Probe #4326 for ge
37	95	4.6	400	22 AAK04398	Human brain expres
38	95	4.6	400	22 AAK29896	Human bone marrow
39	95	4.6	400	22 AAI14482	Probe #4415 for ge
40	95	4.6	400	22 AAI35857	Probe #4543 used t
41	95	4.6	400	22 AAI04308	Probe #4239 used t
42	95	4.6	400	24 ABA04460	Human genome-deriv
43	89.6	4.3	1626	18 AAT88774	Human receptor pro
44	89.6	4.3	1626	20 AAX87651	Human interleukin-
45	89.6	4.3	1626	24 AAD31175	Human IL-18 recept

ALIGNMENTS

RESULT 1	AAS15608	standard; cDNA, 1740 BP.
ID	AAS15608	
XX		
AC	AAS15608;	
XX		
DT	21-MAY-2002	(first entry)
XX		
DE	Human interleukin-1 Receptor accessory protein (IL-1R acp) cDNA.	
XX		
KW	IL-1R acp; human; interleukin-1 receptor accessory protein; NF-kappaB;	
KM	IL-1; IL-1R; ss; inflammatory response.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	10..1722
FT		/*tag= a
FT		/product= "IL-1 Receptor accessory protein"
XX		
XX	US6280955-B1.	
XX		
PD	28-AUG-2001.	
XX		
PF	16-DEC-1997;	97US-0991944.
XX		
PR	16-DEC-1997;	97US-0991944.
XX		
PA	(TUL-) TULARIK INC.	
XX		
XX		
PI	Geo Z;	
XX		


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|||||
Db 61 CAGCTGCATCAAGTCCCACTTTGAACTTTGAAATTCATCTACAGCAGCCCC 120
Qy 185 ATTACGCTGGCTTACTCTGATCTGTATTTGAGTACGAGACCGGACCTTGAAGAGC 244
Db 121 ATTACGCTGGCTTACTCTGATCTGTATTTGAGTACGAGACCGGACCTTGAAGAGC 180
Qy 245 CAATTAACTTCCGCTCCCGGAGAACCGCATTAAGTAAAGAAAGATGTGCTGTGTTCC 304
Db 181 CAATTAACTTCCGCTCCCGGAGAACCGCATTAAGTAAAGAAAGATGTGCTGTGTTCC 240
Qy 305 GGCCCACTCTCTCAATGACACTGGCAACTATTAACCTGCAATGTTAAG 351
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RESULT 9
AA149786
ID AA149786 standard; DNA; 287 BP.
XX
AC AA149786;
XX
Xy 17-OCT-2001 (first entry)
De Probe #8472 used to measure gene expression in human placenta sample.
XX
XX Probe: microarray; human; placenta; antenatal diagnosis;
KW genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00663.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
PA Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-48897/53.
XX
DR Human genome-derived single exon nucleic acid probes useful for
analyzing gene expression in human placenta -
XX
PS Claim 25; SEQ ID No 18472; 654pp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENPs).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders.
XX
XX Sequence 287 BP; 76 A; 78 C; 68 G; 65 T; 0 other;
SO
Query Match 13.9%; Score 287; DB 22; Length 287;
Best Local Similarity 100.0%; Pred. No. 7.7e-81;
Matches 287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 65 AAGCTGCGATGACTGGGAGCTAGACCATGAGCAAAATCCAAAGTTTGAAGATGAGC 124
Db 1 AAGCTGCGATGACTGGGAGCTAGACCATGAGCAAAATCCAAAGTTTGAAGATGAGC 60
Qy 125 CAGCTGCATCAAGTCCCACTTTGAACTTTGAAATTCATCTACAGCAGCCCC 184
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Db 61 CAGCTGCATCAAGTCCCACTTTGAACTTTGAAATTCATCTACAGCAGCCCC 120
Qy 185 ATTACGCTGGCTTACTCTGATCTGTATTTGAGTACGAGACCGGACCTTGAAGAGC 244
Db 121 ATTACGCTGGCTTACTCTGATCTGTATTTGAGTACGAGACCGGACCTTGAAGAGC 180
Qy 245 CAATTAACTTCCGCTCCCGGAGAACCGCATTAAGTAAAGAAAGATGTGCTGTGTTCC 304
Db 181 CAATTAACTTCCGCTCCCGGAGAACCGCATTAAGTAAAGAAAGATGTGCTGTGTTCC 240
Qy 305 GGCCCACTCTCTCAATGACACTGGCAACTATTAACCTGCAATGTTAAG 351
Db 241 GGCCCACTCTCTCAATGACACTGGCAACTATTAACCTGCAATGTTAAG 287

RESULT 10
AA115283
ID AA115283 standard; DNA; 478 BP.
XX
AC AA115283;
XX
Xy 12-OCT-2001 (first entry)
De Probe #5216 for gene expression analysis in human cervical cell sample.
XX
XX Probe: microarray; gene expression; cervical epithelial cell;
KW cervical cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00670.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
PA Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-488901/53.
XX
DR Human genome-derived single exon nucleic acid probes useful for
analyzing gene expression in human cervical epithelial cells -
XX
PS Claim 25; SEQ ID No 5216; 487pp; English.
XX
CC The present invention relates to human single exon nucleic acid probes
CC (SENPs). The present sequence is one such probe. The SENPs are derived
CC from human HeLa cells. The SENPs can be used to produce a single exon
CC microarray, which can be used for measuring human gene expression in a
CC sample derived from human cervical epithelial cells. By measuring gene
CC expression, the probes are therefore useful in grading and/or staging
CC of diseases of the cervix, notably cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 478 BP; 139 A; 105 C; 112 G; 122 T; 0 other;
SO
Query Match 10.7%; Score 220; DB 22; Length 478;
Best Local Similarity 100.0%; Pred. No. 2.8e-59;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 62 CAGAAAGCTGGATGACTGGGAGCTAGACACCATGAGGCAATCCAGTGTGAAAGATG 121
DB 259 CAGAAAGCTGGATGACTGGGAGCTAGACACCATGAGGCAATCCAGTGTGAAAGATG 318
QY 122 AGCCAGCTGGATGACTGGGAGCTAGACACCATGAGGCAATCCAGTGTGAAAGATG 181
DB 319 AGCCAGCTGGATGACTGGGAGCTAGACACCATGAGGCAATCCAGTGTGAAAGATG 378
QY 182 CCCATTGAGCTGGGAGCTAGCTGTGATTTGGATGAGGACCGGACCTTGAGG 241
DB 379 CCCATTGAGCTGGGAGCTAGCTGTGATTTGGATGAGGACCGGACCTTGAGG 438
QY 242 AGCCAAATTAATCTCGGCTCCCGAGAACCGCATTAAGTAA 281
DB 439 AGCCAAATTAATCTCGGCTCCCGAGAACCGCATTAAGTAA 478

ULT 11
36611
AAT36611 standard; DNA; 478 BP.

AC AAT36611;

DT 17-OCT-2001 (first entry)

DE Probe #5297 used to measure gene expression in human placenta sample.

XX Probe: microarray; human; placenta; antenatal diagnosis;
KM genetic disorder; ss.

XX Homo sapiens.

PN MO200157272-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001MO-US00663.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

(MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-488897/53.

PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -

PS Claim 25; SEQ ID NO 5297; 654bp; English.

XX The present invention relates to single exon nucleic acid probes (SENP).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders.

XX Sequence 478 BP; 139 A; 105 C; 112 G; 122 T; 0 other;

QY Query Match 10.7%; Score 220; DB 22; Length 478;

DB Best Local Similarity 100.0%; Pred. No. 2,8e-59; Mismatches 0; Gaps 0;

DB 62 CAGAAAGCTGGATGACTGGGAGCTAGACACCATGAGGCAATCCAGTGTGAAAGATG 121
259 CAGAAAGCTGGATGACTGGGAGCTAGACACCATGAGGCAATCCAGTGTGAAAGATG 318

QY 122 AGCCAGCTGGATGACTGGGAGCTAGACACCATGAGGCAATCCAGTGTGAAAGATG 181
DB 319 AGCCAGCTGGATGACTGGGAGCTAGACACCATGAGGCAATCCAGTGTGAAAGATG 378
QY 182 CCCATTGAGCTGGGAGCTAGCTGTGATTTGGATGAGGACCGGACCTTGAGG 241
DB 379 CCCATTGAGCTGGGAGCTAGCTGTGATTTGGATGAGGACCGGACCTTGAGG 438
QY 242 AGCCAAATTAATCTCGGCTCCCGAGAACCGCATTAAGTAA 281
DB 439 AGCCAAATTAATCTCGGCTCCCGAGAACCGCATTAAGTAA 478

RESULT 12
ABN18246

ID ABN18246 standard; cDNA; 246 BP.

AC ABN18246;

DT 24-JUN-2002 (first entry)

DE Human ORFX polynucleotide sequence SEQ ID NO:4969.

XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
KM hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
KM degenerative disorder; osteoarthritis; neurodegenerative disorder;
KM cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
KM hypertension; hypothyroidism; cholesterol ester storage disease;
KM immune deficiency; immune disorder; infectious disease;
KM autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KM myasthenia gravis; gene; ss.

XX Homo sapiens.

PN WO200192523-A2.

PD 06-DEC-2001.

PF 29-MAY-2001; 2001MO-US10836.

PR 30-MAY-2000; 2000US-206132P.

PR 29-AUG-2000; 2000US-228716P.

PR (CURA-) CURAGEN CORP.

PA Shimkets RA, Leach MD;

DR WPI; 2002-106308/14.

DR P-PSDB; ABP02494.

PT Novel human polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and autoimmune disorders -

PS Disclosure; SEQ ID 4969; 1037bp; English.

XX The present invention describes substantially purified human proteins
CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
CC in the specification)). ABN15762 to ABN27252 encode the human ORFX
CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
CC treating or preventing a pathology associated with an ORFX-associated
CC disorder in humans, and in the manufacture of a medicament for treating a
CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
CC sequences can be used in gene therapy. ORFX sequences can be used in the
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
CC osteoarthritis, neurodegenerative disorders, disorders related to organ
CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
CC storage disease, various immune deficiencies and disorders, infectious
CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
CC disease and autoimmune inflammatory eye disease. ORFX proteins are also

1

Db 737 TGGAGATCAGCCAGTGTATAGATGTCC-----AGCTGGCTAACCCCTGACA 787

QY 791 TTCCCTGATGCTATTTAGTTTCTGATGATCTCGCATGAGTTGTGACCA 850
 Db 788 TCCCTTCGAAGCATTTCTGGATTCAGTGAGAGTCTGGCCCATGATCTACTGATGA 847
 QY 851 TTGATGAAAAAACTGATGACATCTATTTATGTCACATTAAGAAAGTATTAAGTC 910
 Db 848 AAGGAGAAAAATTATTTGAAAGAACCTGACAGGTCACTTAGAAGAGTGAATTAAGGCTTC 907
 QY 911 ATAGTAGAAGAGAGTAAACAGAACTCAGATTTTGAAGATCAAGAAATTTACTCTG 970
 Db 908 TCAAGAGCATCTTGAGAAAAAGAGTTGAGCACTCATCTTTGACTCAGTTGTG 967
 QY 971 AGATCTCAAGCGCAGCTATGCTGTGATGCTAGAAAGTCCAAAGCAAGTTGCCAAAG 1030
 Db 968 AAGCTGACCTGGCAATTTATCTGCAATGTTGAAAACCGAAATGAGAGG-----AAAC 1021
 1031 CAGCGAAGTGAACAGAAAGTCCAGCTCCAGATTAACAGTGAACCTGCTGTGTGTT 1090
 Db 1022 ATGCGCATGTTTCTGCTGTTAAAGATTTAATCTAATAATGAGCTTTCAGGGGGCC 1081
 QY 1091 TTGAGGCAAGTCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 1150
 Db 1082 TGGAGCAATCT 1141
 QY 1151 AGATGCTCTATTTACCGGCTCATTTTGGACAGATGAACCATTTTAGATGGAAG 1210
 Db 1142 AATTGATCT 1201
 QY 1211 AGTATGATTTTATGATCT 1243
 Db 1202 AATATGATGCT 1261
 QY 1244 CGGAGAGAGAGATTTGTATTTACTGACCTCTGCTGAGATTTGGAGATGATTTGGAT 1303
 Db 1262 CTGAGAGAGAGAGATTTGTATTTACTGACCTCTGCTGAGATTTGGAGATGATTTGGAT 1321
 QY 1304 ACAAGCTGATCTTTGACCGGAGAGATGCTGCTGCGGGGAAATACAGTGGAGCAGTTT 1363
 Db 1322 ATTAAGCT 1381
 QY 1364 TTGATTTCT 1423
 Db 1382 CAAGATATGTTGAACAAAGAGAGAGATTTATCTGCTGCTGCTGCTGCTGCTGCTGCT 1441
 1424 AAAAGAGATCAGATGCTGAGTTTAA 1452
 Db 1442 GACGGGAGAGATTTGGAAGTGA 1470
 RESULT 14
 AAD27170
 ID AAD27170 standard; DNA; 2061 BP.
 AC AAD27170;
 XX
 XX 09-APR-2002 (first entry)
 DE Human interleukin-1 receptor DNAX designation 8 (IL-1R8) DNA #2.
 XX
 XX Human; morphogenesis; immune system; interleukin-1 DNAX designation 8;
 KM IL-1R8 protein; therapy; immunological disorder; de.
 XX
 OS Homo sapiens.
 XX
 FT Key Location/Qualifiers
 CDS 1..2061
 FT /*tag= a
 FT /product= "Human IL-1R8 protein"
 XX
 XX US636472-B1.
 PN
 PD 04-DEC-2001.

XX PF 14-OCT-1998; 98US-0173151.
 XX PR 15-OCT-1997; 97US-062066P.
 PR 17-NOV-1997; 97US-065776P.
 PR 18-MAR-1998; 98US-078008P.
 PR 18-MAR-1998; 98US-078416P.
 PR 15-APR-1998; 98US-081883P.
 PR 10-AUG-1998; 98US-095987P.
 XX
 PA (SCHE) SCHERING CORP.
 PI Timans JC, Debets JEMA, Sana TR, Bazan JF, Kastelein RA;
 XX WPI: 2002-121110/16.
 DR P-PSDB; AAE16567.
 XX
 XX Antibody fragments which specifically bind to primate interleukin 1
 PT receptor-like molecules are useful to treat conditions associated with
 PT abnormal expression of the receptor or its ligand, particularly
 PT immunological disorders
 PS disclosure; Column 11-16; 102pp; English.
 XX
 CC The present invention relates to compositions and methods for affecting
 CC mammalian physiology such as morphogenesis of immune system function.
 CC The invention particularly relates to nucleic acids, proteins and
 CC antibodies which regulate development and/or the immune system. The
 CC invention also relates to antibody fragments which specifically bind
 CC to antigenic fragments of a primate interleukin (IL)-1 receptor like
 CC molecules such as IL-1 receptor DNAX designation (IL-1R8). The antibody
 CC fragments of the invention are useful to treat conditions exhibiting
 CC abnormal expression of the receptors or their ligands which typically
 CC will be immunological disorders. The present sequence is a DNA encoding
 CC human IL-1R8 protein.
 XX
 SQ Sequence 2061 BP; 656 A; 421 C; 459 G; 525 T; 0 other;
 Query Match 7.3%; Score 151; DB 24; Length 2061;
 Best Local Similarity 47.4%; Pred. No. 8.5e-37;
 Matches 697; Conservative 0; Mismatches 715; Indels 57; Gaps 6;
 QY 11 TGGGTGTGTAGTGTGATCT 70
 Db 32 TCTGTTCTGTAGTGTGATCT 91
 QY 71 GCGATGACTGGGAGCTAGACACCATGAGGCAATCCAGTGTGTAAGATGAGCAGCTC 130
 Db 92 GCATTTGATGCTGATGATGATCTCAAGCATATCAT---GGCTTGGCAGGTGAACCATGCTC 148
 QY 131 GCATCAAGTCCCATCTCTTTGAACATCTTGAATTCATCTACAGACGACCCATTCAG 190
 Db 149 GAGTGAATGTGCTCTTCT 208
 QY 191 CTGGCTTACTCTGATCTGTGATTTGAGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGG 250
 Db 209 CTGGCTTACTCTGATCTGTGATTTGAGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGG 262
 QY 251 ACTTCCGCTCTCCCGAGAACCGCATTTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 310
 Db 263 TCTTT-----TCAGAGGTCAGATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 316
 QY 311 CTCTCTCTCAATGACATCTGCACTTATCTGATGTTTAAAGAACATCACTATTTGACGA 370
 Db 317 CTGAGGACACAGACAGTGTCTTACATCTGTGTTTAAAGAACATCACTATTTGACGA 376
 QY 371 AAGTTGATTTCTCTGGAAGTTGTTCAAAAAGACAGCTGTTCAATTCCTCCCATGAAC 430
 Db 377 AAGTTGATTTCTCTGGAAGTTGTTCAAAAAGACAGCTGTTCAATTCCTCCCATGAAC 436
 QY 431 TCCAGTGCATTAAGTATATAGATATGACATTAAGAGAGATCACTTGTCCAAATAG 490
 Db 437 TCCGCTATTTAGAAATATGAGATGACATAAAGAGAGAGATCTCTGTCCAGACATG 496


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QY 491 ATGGATATTTTCCTCCAGTGTCAACCGACTATCCTTGATATGGGCTTTATAAA 550
DB 497 ATGACTTAAAAAGCTCCAGACAGAGCTGATGTTGTGTGTATAGAAATGACGCCAA 556
QY 551 TACAGATTTTAAATATGATTAATACCCGAGGATGAACTTGAGTTTCTCATTTAA 610
DB 557 AAATGAGAGAGATTAATATACAGAAAGAAATGCTCTTGATTCAGAAAGTTCAAG 616
QY 611 TTTCAAATTAATGAAATTAACATGTGTTGTAATATCAAGAAATGACGTAAGTTTC 670
DB 617 AAGAGATGAGAGAAATTAACATGTAACCTTAATATGAAAGAAACTTGTAAGCGAA 676
QY 671 ATCTCACAGAGACTCTGACGTGTAAGTATAGGCTCTCCAAAAATGCAAGTCCCTG 730
DB 677 CAATGAAATTAAGATTAAGCTTTACTCAACAGCAAGCTCCCAAGCTATGTTCCCA 736
QY 731 TGATCCATTCACCTAATGATCATGTGCTATGAGAAAGAACGAGAGAGACTCTCA 790
DB 737 TGGAGATACGCCAAGTGTATAGATGTC-----AGCTGGGTAAAGCTCTGAACA 787
QY 791 TTCCTGTACGGTCTATTTTATGTTTCATGATGGAATCTGCAATGAGGTTTGTGACCA 850
DB 788 TCCCTGCAAGAGACTCTTGAGATTCAGTGAAGAGTCTGGGCCAATGATCTACTGATGA 847
QY 851 TTGATGAAAAAAACCTGATGATCATCTATTGATGTCACCTTAACGAAAGTAAATGTC 910
DB 848 AAGAGAGAAAGTATTAATTAAGAACTGCGAGGTCACTTAAGAGAGGTAATAGGCTTC 907
QY 911 ATGTAAGAACAGAGATGAACAAAGACTCAGATTTTGAGATCAAGAAAGTTACCTCG 970
DB 908 TCAAGAGACTCTTGAGAGAAAGAAAGATTAATGATGCACTCATCTTTGACTGAGTTGG 967
QY 971 AGGATCTCAAGCGAGCTATGTCTGTCATGCTAGAGTCCCAAGGCAAGTTGCCAAG 1030
DB 968 AAGCTGACTGGGCAATTAATACCTGCGATGTGAAACCGAAATGACGG-----AAAC 1021
QY 1031 CAGCCAGGTGAAGCAGAAAGTGCAGCTCCAGATACAGATGAGCACTGGCTTGTGCTT 1090
DB 1022 ATGCGAGTGTGTTGCTCGTAAAGAAAGATTAATCTAATTAATTAAGCTTGCAGGGGCC 1081
QY 1091 TTGAGCGCAGATCTCTAGTGTGATTTCTCATTTGTTTACCATGTTTACTGCTAG 1150
DB 1082 TGGAGAGAACTCTCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1141
QY 1151 AGATGCTCTAATTTTACCGGCTCATTTTGACAGATGAAACCAATTTTGAAGGAAAG 1210
DB 1142 AATTGATGCTCTCTCTACAGGAGACATTTGAGCTGATGAATGAATGACAAAGG 1201
QY 1211 AGATGATTTATTAATTAATCTCTATGCAAG-----AATG 1243
DB 1202 AATATATGCTCTCTCTCTCTCTTACCAAAAGTGAACAAATTAATTAAGCTGACATC 1261
QY 1244 CGGAGAGAGAAATTTGATTAATCTGACCTCGTGAAGTTTGGAGATTAATTTGAT 1303
DB 1262 CTGAGAGAGAGAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1321
QY 1304 ACAAGCTGTGATCTTTGACCGGAGAGAGCTGCTGCGGGGAAATATACGTGAGACGTTT 1363
DB 1322 ATAAACTCTTCATCCAGAAAGAGACCTGATTCAGAGTGAACATACATGAGAAATCTCA 1381
QY 1364 TTGATTTTATTCAGAGAGAGAGAGATGATGTTGTTCTGAGGCTGACATATGACAG 1423
DB 1382 CAAGATATGTTGAACAGAGAGAGACTTATTAATGCTGCTAATCTCCAGACTATATCTCA 1441
QY 1424 AAAAGACATCAGCATGCTGAGTTTAA 1452
DB 1442 GACGGGATGAGATTTTTCGAACTGGA 1470
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RESULT 15
ABA50826
ID ABA50826 standard; DNA; 169 BP.

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XX AC ABA50826;
XX DT 01-FEB-2002 (first entry)
XX DE Human breast cell single exon nucleic acid probe #9521.
XX KW Human; microarray; single exon probe; gene expression; breast;
XX KW disease; cancer; ss.
XX OS Homo sapiens.
XX PN W0200157271-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US00662.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SQ, Hanzel DK, Chen W, Rank DR;
XX DR MPI; 2001-496933/54.
XX PT New spatially-addressable set of single exon nucleic acid probes,
XX PT useful for measuring gene expression in sample derived from human
XX PT breast, comprises number of single exon nucleic acid probes
XX PS Claim 4; SEQ ID NO 9521; 327bp + sequence listing; English.
XX CC The invention relates to a spatially-addressable set of single exon
XX CC nucleic acid probes for measuring gene expression in a sample derived
XX CC from human breast and BT 474 cells. The method involves contacting
XX CC the probes with a collection of detectably labelled nucleic acids
XX CC derived from mRNA of human breast, and then measuring the label
XX CC bound to each probe of the microarray. The probes are useful for
XX CC verifying the expression of regions of genomic DNA predicted to
XX CC encode proteins. They are useful for gene discovery, and for
XX CC determining predisposition and/or prognosing breast disease. Gene
XX CC expression analysis is useful for assessing the toxicity of chemical
XX CC agents on cells. The microarray of this invention presents a far greater
XX CC diversity of probes for measuring gene expression, with far less bias
XX CC than expressed sequence tag microarrays. The method is suitable for
XX CC rapid prediction of functional information from genomic sequence. The
XX CC present sequence is a single exon nucleic acid probe of the invention.
XX CC Note: The sequence data for this patent did not form part of the
XX CC printed specification, but was obtained in electronic format directly
XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
SQ Sequence 169 BP; 62 A; 29 C; 44 G; 34 T; 0 other;
Query Match 7.2%; Score 149; DB 22; Length 169;
Best Local Similarity 100.0%; Pred. No. 6.7e-37;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 903 TATATAGTATAGTAGAAGAGAGATGAACAAAGAACTCAGATTTTGAGCATCAAGAAAT 962
DB 1 TATATAGTATAGTAGAAGAGAGATGAACAAAGAACTCAGATTTTGAGCATCAAGAAAT 60
QY 963 TACCTGAGAGATCTCAAGCGAGCTATGCTGTAATGTATAGAGCCAAAGCGGAAGT 1022
DB 61 TACCTGAGAGATCTCAAGCGAGCTATGCTGTAATGTATAGAGCCAAAGCGGAAGT 120
QY 1023 TGCCAAAGCGCAAGGTGAAGCAAGAAAG 1051
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Thu May 1 09:36:46 2003

us-10-061-727-1.rng

Page 15

Db 121 TGCCAAAGCAGCCAAAGGTGAAGCAGAAAG 149

Search completed: April 30, 2003, 08:04:12
Job time : 328 secs

TELEFAX: (650) 343-4342
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3355 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 135..1844
 US-08-991-944-3

Query Match 51.7%; Score 1067.4; DB 4; Length 3355;
 Best Local Similarity 78.9%; Pred. No. 0;
 Matches 1298; Conservative 0; Mismatches 341; Indels 6; Gaps 2;

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1 ATGACACTTCTGTCGTGTGATGAGTCTCTACTTTTATGGAATCTGCAAAAGTATGCC 60
135 ATGGAGCTCTGTGTGATGAGTCTCTCTCTATGAGGATCTGCAAGATCATGCT 194
61 TCAGAACGCTGCGATGAGTCTGCGGAGCTAGACACATGAGGCAATCCAAAGTTGAAGAT 120
195 TCGAGGCGCTGTGTGATGAGTCTGCGGAGCTAGATACATGAGGCAATCCAAAGTTGAAGAT 254
121 GAGCCAGCTGCGATGAGTCTGCGGAGCTAGATACATGAGGCAATCCAAAGTTGAAGAT 180
255 GAGCCAGCTGCGATGAGTCTGCGGAGCTAGATACATGAGGCAATCCAAAGTTGAAGAT 314
181 GCGCATTCAGCTGCGCTTACTCTGTATGATGATGATGATGATGATGATGATGATGATGAT 240
315 GCGCATTCAGCTGCGCTTACTCTGTATGATGATGATGATGATGATGATGATGATGATGAT 374
241 GAGCCAGTAACTTCTGCGCTTACTCTGTATGATGATGATGATGATGATGATGATGATGAT 300
375 GAGCCAGTAACTTCTGCGCTTACTCTGTATGATGATGATGATGATGATGATGATGATGAT 434
301 TTCGCGGCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
435 TTCGCGGCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 494
361 TATTCGAGCAAGTGTGATTTTCCCTGGAAGTTGTTCAAAAAGACAGCTGTTCAATTCC 420
495 TATTCGAGCAAGTGTGATTTTCCCTGGAAGTTGTTCAAAAAGACAGCTGTTCAATTCC 554
421 CCCATGAACTCCCAAGTGAATATGATGATGATGATGATGATGATGATGATGATGATGAT 480
555 GCGATGATTTCCCAAGTGAATATGATGATGATGATGATGATGATGATGATGATGATGAT 614
481 CCAATGATGATGATGATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
615 CCAATGATGATGATGATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 674
541 TGTATTAATAATGATGATTTTAAATGATGATGATGATGATGATGATGATGATGATGATGAT 600
675 TGTATTAATAATGATGATTTTAAATGATGATGATGATGATGATGATGATGATGATGATGAT 724
601 ATTGCTTAAATGATGATTTTAAATGATGATGATGATGATGATGATGATGATGATGATGAT 660
735 ATCCCTTGTGATGATTTTAAATGATGATGATGATGATGATGATGATGATGATGATGATG 794
661 CGTACGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
795 CGTACGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 854
721 GTGCCCCCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
855 TTGCGCAACCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 914
781 GAGCTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
915 GAACTGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 974
  
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841 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
975 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1034
901 AGTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
1035 AGTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1094
961 GTTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
1095 GTTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1154
1021 GTTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
1155 GTTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1214
1081 GCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
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1141 TACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
1275 TACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1334
1201 GATGAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
1335 GATGAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1394
1261 GTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
1395 GTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1454
1321 GATGAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
1455 GATGAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1514
1381 AGCAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
1515 AGCAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1574
1441 CTGAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1497
1575 CTGAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1634
1498 GTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1557
1635 GTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1694
1558 ---TCTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1614
1695 CTGAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1754
1615 GCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1639
1755 GCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1779
  
```

RESULT 3
 US-09-173-151A-3
 Sequence 3, Application us/09173151A
 Patent No. 6326472
 GENERAL INFORMATION:
 APPLICANT: Timans, Jacqueline C.
 APPLICANT: Debeets, Johannes Eduard Maria
 APPLICANT: Antonius
 APPLICANT: Sana, Theodore R.
 APPLICANT: Bazu, J. Fernando
 APPLICANT: Kastelein, Robert A.
 TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods.
 NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:
 ADDRESSER: DNAX Research Institute
 STREET: 901 California Avenue

Oy 1364 TTGATTCTAGAGACGAGAGATATTGTTCTGAGCCCTGACTGATGACAG 1423
 Db 1382 CAAGATATCTTGAACAAGAGAGACTTATTCGTGCTAACTCCAGACTATATCTCA 1441
 Oy 1424 AAAAGAGATCGAGATGCTGAGCTTTAA 1452
 Db 1442 GAGGGGATGAGTATTTTCGAACTGAA 1470

RESULT 4

US-09-173-151A-34
 Sequence 34, Application US/09173151A
 Patent No. 6326472

GENERAL INFORMATION:

APPLICANT: Timans, Jacqueline C.
 APPLICANT: Debets, Johannes Eduard Maria
 APPLICANT: Antonius
 APPLICANT: Sana, Theodore R.
 APPLICANT: Bazan, J. Fernando
 APPLICANT: Kastelein, Robert A.
 TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
 NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:
 ADDRESS: DNAX Research Institute
 STREET: 901 California Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/173,151A
 FILING DATE: 14-OCT-1998
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/065,776
 FILING DATE: 17-NOV-1997

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/078,008
 FILING DATE: 12-MAR-1998

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/081,883
 FILING DATE: 15-APR-1998

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/095,987
 FILING DATE: 10-AUG-1998

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/078,416
 FILING DATE: 18-MAR-1998

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/062,066
 FILING DATE: 15-OCT-1997

ATTORNEY/AGENT INFORMATION:
 NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DX0767X

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650)852-9196

TELEFAX: (650)496-1200

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 2537 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..2004

US-09-173-151A-34

Query Match 7.0%; Score 144.4; DB 4; Length 2537;
 Best Local Similarity 46.2%; Pred. No. 1.9e-36;
 Matches 640; Conservative 0; Mismatches 701; Indels 45; Gaps 3;

Oy 94 ATGAGCAATTCAGAGTGTGTAAGATGAGCCAGCTGCATCAAGTCCACTTTTGA 153
 Db 28 ATCAGAAATATCAAGTTTGTGTGAGAGAGCTGTGCAATCAATATGACCTTTTAT 87
 Oy 154 CACTTCTGAAATTCACATCAAGACAGCCCATTCAGCTGCTTACTGTCTGTAT 213
 Db 88 GGTATATCAGAAATTAATCTCCCTTCGCAAGTGTGACTGATGATGATGATG 147
 Oy 214 TGGACTAGGAGAGAGCCGAGCTTGTGAGGCAATTAATCTCCGCTCCGAGAACGC 273
 Db 148 AAAGTTCTGCTCTGAGAGACTTGAAGAGCCAAATAGCT-----TTAGAGAGTGA 201
 Oy 274 ATTAGTAAGAGAAAGATGTGTGTGTCGCGCCACTCTCTCTCAATGACACTGCAAC 333
 Db 202 ATGACCAAGAGAAAGATCCATTTGTTTGGGCAATTTGCTACAGGAGTGTCTC 261
 Oy 334 TATACCTGCATGTAAAGAACATACATATTTGACAGCAAGTTGCATTTCTTGAAGTT 393
 Db 262 TACGCTGTGATCAGAGACTCCACTTACTGTATGAAGATCCATCTCAGACAGTG 321
 Oy 394 GTTCAAAAAGACGCTTTTCAATTCCTCCCAATGAACTCCAGTGCATTAATGATATA 453
 Db 322 GGTGAAATGACACTGAGCTGTCTATTAATCCAGATGAAGATTTTGAAGAACTGA 381
 Oy 454 GAATATGCAATTCAGAGATCACTGTCCAAATGATATATTTTCTCCAGTGC 513
 Db 382 CTAGCAAAAGAGAAATTTTATGCTGCTGATGAGATTTTCTATGCAACGACA 441
 Oy 514 AAACGACTATCACTGTGTATATGCGCTGTATTAATTAATGAAATTTAATATGTA 573
 Db 442 GAACCTGAATCTCTTGTGTAAGAGATGAGAGACAAAGATGAGGCAAGTATGTA 501
 Oy 574 CCGGAGGTATGAACTTGAAGTTTCTCATGCTTAAATTTCAAATTAATGAAATTTACA 633
 Db 502 TTCAAAAGAGATCTCTCTTATTAAGAGATGAGAGATGACATTTGAAATTAATACC 561
 Oy 634 TGTGTTGTTACATATCCAGAAATGAGAGTACGTTTCACTCAGAGACTGTGTA 693
 Db 562 TGTGAATTAATATATGAG-----GTTTGTGTGAGAGAACTACTGAATTA 609
 Oy 694 AAGGTATGAGCTTCCAAAATGCAAGTCCCTGTGATTCATTCATTAATGATCAT 753
 Db 610 ACTGTACAGCCCTCTGATGATGATGACCAAGCTTTGTATCTATGGAAGTAA 669
 Oy 754 GTGTCTATGAGAAAGAACAGAGAGAGTACTCATTTCCCTGTACGCTATTTTACT 813
 Db 670 CTGACAAATTCAGAGACCCAGCTGTGTGATCTGTGATTAATCCCTGCAAGACTTTCTT 729
 Oy 814 TTTGATGAGATTCGCAATGAGGTTTGTGACCATTTGAGAAAGAAATCTGATGAC 873
 Db 730 GGGTACAGCGAGATGTGATCTCTTTAATTTAATGAGAAAGAGAAATTTTATGAA 789
 Oy 874 ATCATTATGATGTCCACCATTAACAAAGTATTAATGATGAGAAAGAGAAATCA 933
 Db 790 GATCGATGAAATATGAGATTTGGGAAAGTACATTAATTTAAGAGATCTGTGG 849
 Oy 934 AGAATCTGATTTTGAAGATCAAGAAATTTACTTGTGAGATCTTAAGCGCAGTATGTC 993
 Db 850 GAACAGAGATTTCCATCTCATTAATTTGTGCTCTGTGAGAGAGAGTACATTTGGAAT 909
 Oy 994 TGTATGTAGAGAGCAAGGCGAAGTGTCCAAAGCAAGCAAGGTAGAGAGAAAGT 1053
 Db 910 TACTCTGTATATGTTGAAATGAAATGAGATGAGATGAGACAGCGAGCTTCTCTTATATA 969
 Oy 1054 CCAGCTCCAAATACAGAGTGAAGTGTGTTTGTGAGAGCAAGTCTGCTAGTG 1113
 Db 970 CGAGAGCTATATGATACAGAGTGAAGTGTGAGAGCTTGTGATTAATCTTGTGCTT 1029

Page 6

APPLICATION NUMBER: US 60/078,416

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      FILING DATE: 18-MAR-1998
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 60/062,066
      FILING DATE: 15-OCT-1997
      ATTORNEY/AGENT INFORMATION:
      NAME: Ching, Edwin P.
      REGISTRATION NUMBER: 34,090
      REFERENCE/DOCKET NUMBER: DX067X
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (650)852-9196
      TELEFAX: (650)496-1200
      INFORMATION FOR SEQ ID NO: 1:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 1737 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: cDNA
      HYPOTHEICAL: YES
      FEATURE:
      NAME/KEY: CDS
      LOCATION: 1..1737
      FEATURE:
      NAME/KEY: misc feature
      LOCATION: 342..343
      OTHER INFORMATION: /note= "splice junction"
      FEATURE:
      NAME/KEY: misc feature
      LOCATION: 453..454
      OTHER INFORMATION: /note= "splice junction"
      FEATURE:
      NAME/KEY: misc feature
      LOCATION: 756..757
      OTHER INFORMATION: /note= "splice junction"
      FEATURE:
      NAME/KEY: misc feature
      LOCATION: 885..886
      OTHER INFORMATION: /note= "splice junction"
      FEATURE:
      NAME/KEY: misc feature
      LOCATION: 1033..1034
      OTHER INFORMATION: /note= "splice junction"
      FEATURE:
      NAME/KEY: misc feature
      LOCATION: 1177..1178
      OTHER INFORMATION: /note= "splice junction"
      FEATURE:
      NAME/KEY: misc feature
      LOCATION: 1350..1351
      OTHER INFORMATION: /note= "splice junction"
      US-09-173-151A-1
      Query Match      6.8%; Score 139.4; DB 4; Length 1737;
      Best Local Similarity 47.8%; Pred. No. 6.3e-35;
      Matches 678; Conservative 0; Mismatches 681; Indels 60; Gaps
      7;
      64 GAACCTGCAGTGACTGGGGAAGTGAACCACTGAGGCAATCCAAAGTTGGAAGATGAG 123
      70 GATGCTGCAGTGAAGTGCCTTTCTTCAAGTTATTTGTTACCACTATAGCAAGGCC 126
      124 CCGAGCTGCAGTGAAGTGCCTTTCTTGAACACTTCTTGAATTTCACTAGACAGGCC 183
      127 CCAATCCGAAGTGAAGTGCCTTTCTTCAAGTTATTTGTTACCACTATAGCAAGGCC 186
      184 CATTCACTGCCTTACTTCTGATCTGGTATTTGAAGTGAAGGACCGGACCTTGAGAG 243
      187 CAGAGCACTGGGCTCAGGCTTATGTGTACAAAC-----AAGGATTTGGAAGAG 240
      244 CCAATTACTTCGGCTTCCCGAGAACCGCATTTATGTAAGGAAAGATGTCTGTGTTTC 303
      241 CCCATCATCT-----TTTCAAGAGGTGAGATGCAAGGAAATTCATATATGTTT 294
      304 CGGCGCACTCTCTCATATGACATGGCACTATCTGCAATGTTAAGGAACATACATAT 363

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Db 295 CACTACCTGAGGCAAGAGATGATTTCTACCTGTGTTTAAAGAACTCAACATAT 354
Qy 364 TGACAGAAAGTGTGATTTCCCTTGAAGTTGTTCAAAAAGACAGCTGTTCAATTTCCCC 423
Db 355 TGATGAAAGTGTCAATGTCTTTCATCTTTCAGAGAAATGAAATGAGCCCTGTACAC 414
Qy 424 ATGAACTCCAGTGATAACTGTATATAGAAATAGGCAATTCAGAGATCACTGTCCA 483
Db 415 AGCAGATCCGCTATTTAGAAAATTCGAAGTCACTAAAAGAAAGAGATCTCTGTCCA 474
Qy 484 AATGTATAGATATTTTCTTCCAGTGTCAAAACCACTATCACTGTATATGGCTGT 543
Db 475 GACATGATATCTTTAAAGTCCGATCAGAGCTGATGTGTGTATAGAAATGAC 534
Qy 544 TATATAATACAGATTTTAAATATGTAATCCGAGATATGAACTTGATTTCTCAT 603
Db 535 AAGCAAAAATGTGAGAGATATATATACGAAAGAAATGCTCTTGTGATCAAGAA 594
Qy 604 GCCTTAATTTCAATATATGAAATATACATGTGTGTATCATATCCAGAAATGACGT 663
Db 595 GTTCAAGAGATGAGAGAAATTTACATGATGACTTAAATATGAGAGAAATCTGTA 654
Qy 664 ACCTTATATCTACAGAGATCTGACTGTAAAGTATAGGCTCTCCAAAATGCACTG 723
Db 655 AGACGAACTGATTTGAAAGTAAAGTAACTTACTCAGACAGCCCTCCAAAGCCAT 714
Qy 724 CCCCCTGTATCACTTCACTTAATGATCATGTGTCTATGAGAAAGAACGAGAGAG 783
Db 715 TTCCCATGAGATCAAGCAAGTATATATGATATC-----CAGCTGGGTAACCT 765
Qy 784 CTAATCTTCCCTGTACGCTATATTTAGTTTCTGATGATCTCCCAATGAGAGTTGG 843
Db 766 CTGAACATCCCTGTCAAGATCTTGTGATGATGAGATGAGTGTGGCCATGATCTAC 825
Qy 844 TGACCAATGATGAGAAAAAACTGATGATCACTATGATGATGATGATGATGATG 903
Db 826 TGATGAAAGAGAGAAAGTTATGAAAGATCTGAGAGATGATGAGAGAGATGAT 885
Qy 904 ATAGATATGATGAAAGAGATGAAAGAACTGATGATGATGATGATGATGATGAT 963
Db 886 AGCTTCTCAAGAGATCTTGTGAGAAAGAAATGATGATGATGATGATGATGATG 945
Qy 964 ACCTGATGATCTCAAGCAGATGATGATGATGATGATGATGATGATGATGATG 1023
Db 946 GTTGTGAAAGCTGACCTGGGAAATTAATCTGCATG-----TTGAAACCGAAATGA 999
Qy 1024 GCCAAAGCAGCAGATGAAAGAGAAAGTCCAGCTCAAGATACAGATGAACTGG 1083
Db 1000 CGGAAACATGCTCAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1059
Qy 1084 TGTGTTTGTGAGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1143
Db 1060 GGGGGCTGTGAGCAATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1119
Qy 1144 TGGCTAGAGATGATCTTATTTTACCGGGCTCATTTTGAACAGATGAAACCATTTG 1203
Db 1120 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1179
Qy 1204 GGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1239
Db 1180 AACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1239
Qy 1240 ---AATGCGAAGAGAGAAATTTGATGATGATGATGATGATGATGATGATG 1296
Db 1240 GACATGCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1299
Qy 1297 TTTGATATCAAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1353
Db 1300 TATGATATTAATCTTCTATCTCCAGAAAGAGAGAGAGAGAGAGAGAGAGAG 1359
Qy 1354 GAAGCAGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1413

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Db 1360 GAAGATCTCAAGATATGTTGTAACAAGACAGAACTTATATCTGCTACTCCAGAC 1419
Qy 1414 TATGTGACAGAAAAGACATCAGAGTGTGAGATTAA 1452
Db 1420 TATATTTCAAGCGGGATGAGATATTTTGAAGTGA 1458

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RESULT 6

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US-08-604-333-1
; Sequence 1, Application US/08604333
; Patent No. 5776731

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GENERAL INFORMATION:

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; APPLICANT: Parnet, Patricia et al.
; TITLE OF INVENTION: Receptor Designated 2P1
; NUMBER OF SEQUENCES: 5

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CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101

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COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a

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CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/604,333
; FILING DATE: 21-FEB-1996

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CLASSIFICATION:

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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2619
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822

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INFORMATION FOR SEQ. ID NO. 1:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1626 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: hu2F1

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FEATURE:

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; NAME/KEY: CDS
; LOCATION: 1..1626
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: 58..1623
; NAME/KEY: sig peptide
; LOCATION: 1..57

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US-08-604-333-1

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Query Match 4.3%; Score 89.6; DB 1; Length 1626;
Best Local Similarity 46.3%; Pred. No. 1,1e-18;
Matches 391; Conservative 0; Mismatches 423; Indels 24; Gaps 2;

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Qy 604 GCCTTAATTTCAATATATGAAATATACATGTGTGTATACATATCCAGAAATGACGT 663
Db 523 GCGAGTTTGAAGATCAGGGGATATATCTCTGCGCATTTCTCTCATATATGAAAA 582
Qy 664 ACCTTATATCTCAAGCACTGACTGTAAAGATGATGATGATGATGATGATGATG 723
Db 583 CTATTTAATATCAACAACTTCAATATATACAAATGATGAGAGATGCGATATATG 642

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TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1563 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: mat peptide
 LOCATION: 1..1563
 IDENTIFICATION METHOD: E
 US-08-996-338-1

Query Match 3.6%; Score 75.2; DB 3; Length 1563;
 Best Local Similarity 46.1%; Pred. No. 5.5e-14;
 Matches 389; Conservative 0; Mismatches 428; Indels 27; Gaps 3;

QY 604 GCCTTAATTCATTAATGAAATTAACATGATGTTGTTCAATATCCAGAAATGAGCGT 663
 DB 466 GCCGAGTTTAAGATCGAGGGATTTACTCTCGGTCATTTCTTCAATATGAGAAA 525
 QY 664 ACCTTCATTCACACAGACTCTGATGTAAGGTAGTACGCTCTCCAAAAATGCAGTG 723
 DB 526 CATTTAATATCAACAAAACCTTCAATATACATAGTGAAGATGCCAGTATATAGTT 585
 QY 724 CCCCCTGATCCATTCATCACTTAATGATGCTCTATGAGAAACACAGAGAGAG 783
 DB 586 CCGGTCTCTTGGACCAAGACTTAACCATGTTGCAGTGAAATTAGAAAAACGTAAG 645
 QY 784 CTACTATTCCTGTAAGGCTATTTTATGTTTCTGATGATTCCTGCAATGAGTTTG 843
 DB 646 CTAACTGCTCTGCTTCTGTAATGAAAGAGATGTAATTTATGATGTTGCGAGAA 705
 QY 844 TGACCATTCATGAAAAAAACCTGATGATCATATGATGTCACATTAACGAAAGT 903
 DB 706 AATGATCGATCTCTAATATACATGAGAAAGAAATGAAATGATATGATCCAGAGGC 765
 QY 904 ATATGATCATATGTAACAGAAATGAAACAAACTCAGATTTTGGATCAAGAAAGTT 963
 DB 766 AATGATCATGCTTCAAAAGATTTGAGAAATGAAATATTTGTTGAAACATCTAAATGTT 825
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 DB 826 TTAATATATTTGCACTGTCGACGACGAGGAGGACACAGACCCAAAGCTTCATTTGT- 884
 QY 1024 GCCAAGCAGCCAGGTGAAAGCAAAAGTCCAGCTTCAAGATACACAGTGAAGTGGCT 1083
 DB 885 -----GAGAAAGACATGCTGATATCCAGCCACGCTTCAAGAGGAAATGATCA 937
 QY 1084 TGTGTTTTGGAGCCACAGTCTGCTAGTGTGATTCATATGTTGTTTACCATGTTTAC 1143
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 QY 1249 GAAGAAAGATTTGATTTACTGACCTTCCTGAGATTGAGAAATGAAATTTGATGTAAG 1308
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 QY 1309 CTGTGATCTTTGACGAGACATGCTGCTGGGGGAAATACATGAGAGAGATTTTATGAT 1368
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 QY 1369 TTCAATTCAGAGAAAGAGATGATGTTGTTCTGAGCCCTGATGATGACAGAAAG 1428

DB 1234 CTGATAGAGAAAGCCGAGACTAATCATGCTCTAATGTAAGTATATGCTAATGAG 1293
 QY 1429 AGCA 1432
 DB 1294 GTCA 1297

RESULT 11
 US-08-996-338-7
 ; Sequence 7, Application US/08996338
 ; Patent No. 6087116
 ; GENERAL INFORMATION:
 ; APPLICANT: TORIGOE, Kakuji
 ; APPLICANT: OKURA, Takamori
 ; APPLICANT: KURIMOTO, Masashi
 ; TITLE OF INVENTION: POLYPEPTIDES
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWDY AND NEIMARK
 ; STREET: 419 Seventh Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/996,338
 ; FILING DATE: 22-DEC-1997
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: JP 74,697/1997
 ; FILING DATE: 12-MAR-1997
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: JP 215,486/1997
 ; FILING DATE: 28-JUL-1997
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: JP 291,837/1997
 ; FILING DATE: 09-OCT-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BROWDY, Roger L.
 ; REGISTRATION NUMBER: 25,618
 ; REFERENCE/DOCKET NUMBER: TORIGOE=3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-628-5197
 ; TELEFAX: 202-737-3528
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1620 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; ORIGINAL SOURCE:
 ; ORGANISM: lymphoblastoid cell derived from a patient
 ; ORGANISM: with Hodgkin's disease
 ; INDIVIDUAL ISOLATE: L428 (PERM BP-5777)
 ; FEATURE:
 ; NAME/KEY: sig peptide
 ; LOCATION: 1..57
 ; IDENTIFICATION METHOD: E
 ; FEATURE:
 ; NAME/KEY: mat peptide
 ; LOCATION: 58..1620
 ; IDENTIFICATION METHOD: E
 ; US-08-996-338-7

Query Match 3.6%; Score 75.2; DB 3; Length 1620;
 Best Local Similarity 46.1%; Pred. No. 5.7e-14;
 Matches 389; Conservative 0; Mismatches 428; Indels 27; Gaps 3;

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Oy	724	CCCCGTGATCCATTCACCTAATAGATCATAGTGTCTATAGAAAATAACACAGAGAGAG	783
Db	643	CCGGTTCTTCTTGGACCAAAAGCTTAACCATATGTCAGTGGATTTAGAAAAAAACCTAAGG	702
Oy	784	CTACTCATTCCTCTGATCGGTCTATTTTAGTTTTCTGATGGAATTTCCGCAATGAGGTTGG	843
Db	703	CTCAACTGCTCTGCTTTGCTGAATGAAGAGATGTATTTATTTAGATGTTCGGGGAGAA	762
Oy	844	TGGAACATTGATGAAAAAAACCTGATGACATCATATTTGATGTCAACCTTAACGAAGT	903
Db	763	AATGATTCGATCTTAATATATACATGAAGAAAAAGAAATGAGATTTATGCTCCAGAGGC	822
Oy	904	ATAAGTCATAGTACACAGAAAGATGAAACAAAGACTCAATTTTGACATCAAGAAAGTT	963
Db	823	AAATGCAATGCTTAAAAAGTATTTGAGATTGAAAATTTGTGTAAAGCAATCTAAATGTT	882
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Db	995	TAGCTGTTTGCATC-----TTGTGTGACGATAGTGTGCTTAGTGAATCTGTGTGTCAATTAAT	1055
Oy	1144	TGCGTAGAGATGTCCTATTTTAAACCGGACTCATTTTGGAAACAGATGAAACATTTTAGT	1203
Db	1051	AGAGTTGACTTGGTTCTTAATTTTATAGCATTTTAACGAGAGAGATGAAACATTTAACAT	1110
Oy	1204	GGAATAAGATATGATTTATTTATATCTTATGCAA-----GGAATGCGGA	1248
Db	1111	GGAATAACATATGATGCTTTTGTGTCTTAACTTAAAGATGCGGACCTGAAAAATGAGAG	1170
Oy	1249	GAAAGAAATTTGATTAATCACTGACCCCTCGTGAGTTTGGAGATGAATTTGGATATCAAG	1308
Db	1171	GAGCAACACTTTGCTGTGAGAAATTTTCCAGAGGTGTGGAGAAACATTTTGGGTATAG	1230
Oy	1309	CTGTGCATCTTTGACCGAGACAGTCTGCCCTGGGGGAAATPACGTGGACACAGTTTGTAT	1366
Db	1231	TTATAGCATATTTGAAGGAGATGATGTCCTGAGAGAGCTGTGTATATATAATATCACTCA	1290
Oy	1369	TTCAATTCAGAGACAGAGGATGATGTGTCTGAGCCCTGACTATGTGACAGAAAG	1428
Db	1291	CTGATAGAGAAATACCGAAGACTAATCATTTGTCTTAAGTAAAGTATATATGTCTATAGG	1355
Oy	1429	AGCA	1432
Db	1351	GTCA	1354

RESULT 12
 US-08-996-338-2
 : Sequence 2, Application US/08996338
 : Patent No. 6087116
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 : GENERAL INFORMATION:
 :
 : APPLICANT: TOPICOE, Kakui
 : APPLICANT: OKURA, Takaochi
 : APPLICANT: KUNIMOTO, Mutsashi
 : TITLE OF INVENTION: POLYPEPTIDES
 :
 : NUMBER OF SEQUENCES: 37
 :
 : CORRESPONDENCE ADDRESS:

```

ADDRESS: BROWDY AND NEWMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,338
FILING DATE: 22-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74,697/1997
FILING DATE: 12-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 215,488/1997
FILING DATE: 28-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 291,837/1997
FILING DATE: 09-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOE=3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1557 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: mat peptide
LOCATION: 1..1557
IDENTIFICATION METHOD: S
US-08-996-338-2

Query Match 3.5%; Score 73; DB 3; Length 1557;
Best Local Similarity 54.2%; Pred. No. 2.9e-13;
Matches 148; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

QY 1182 AACGATGAAACATTTTAGATGAAAGAGATGATATTATGTATCTATGCAAGAA 1241
      |||||
Db 1044 AACGATGATAAACATATGATGCTTTGTGTCTTACCTGAAAGTGTCTATCTGAA 1103
      |||||
QY 1242 TGGCGAAGAGAAATTTGTATTAAGTACCCCTCGTGAAGTTTGGAGAAATTTGG 1301
      |||||
Db 1104 TAAAGAAAGATATCTTTGCTGTGAGACCTTACCCAGGCTCTGAGAAACAGTTGG 1163
      |||||
QY 1302 ATACAGCTGTGATCTTTTGAACCGAGACAGTCTGCTCGGGGAAATATACATGGAAGCAGT 1361
      |||||
Db 1164 GTATTAAGTTATGATATTTGAAAGAGATGTGTGCTCGGGGAGACTGTTCGAGAGAT 1223
      |||||
QY 1362 TTTTGAATTTATTAGAGAAACAGAGATGATTTGTTCTGAGCCTGACTATGTGAC 1421
      |||||
Db 1224 CCATTCATCTGATAGAAAGAACCCGAGGCTATATCATGTTCTCGACGAGATTAAGTAC 1283
      |||||
QY 1422 AGAAAGAGCATGACATGCTGAGATTAAACT 1454
      |||||
Db 1284 TACCGAGCCAGGCGTGAAGCTCGAGAGTGAAGT 1316
      |||||

RESULT 13
US-08-604-333-3
; Sequence 3, Application US/08604333.
; Patent No. 5776731
; GENERAL INFORMATION:

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APPLICANT: Parnet, Patricia et al.
TITLE OF INVENTION: Receptor Designated 2F1
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/604,333
FILING DATE: 21-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2619
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2830 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: mu2F1
FEATURE:
NAME/KEY: CDS
LOCATION: 381..1994
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 435..1991
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 381..434
-08-604-333-3
Query Match 3.5%; Score 73; DB 1; Length 2830;
Best Local Similarity 54.2%; Pred. No. 4.4e-13;
Matches 148; Conservative 0; Mismatches 125; Indels 0; Gaps 0;
Qy 1182 AACAGATGAACCATTTAGATGGAAGAAAGATATTTATGATCTATGCAAGAA 1241
Db 1478 AACAGATGTAACCATATATATGCTTTGTCTTACCTGAAGAGTATCTGAGAA 1537
Qy 1242 TCGGGAAGAAGAAATTTGTATTACTGACCCCTCGGAGTTTGAAGAAATTTGG 1301
Db 1538 TAAAGAGAGTATATCTTTCTGAGAGCTTACCCAGGCTCTGGAAGAAACAGTTGG 1597
Qy 1302 ATACAGCTGTGATCTTTGACGAGACAGTCTGCGGGGAATACAGTGAAGCAGT 1361
Db 1598 GTATTAAGTATGATATTTGAAGAGATGTGTGCTGCGGAGCTGTGTCGAGAGAT 1657
Qy 1362 TTTTGAATTCATTCAGAGAGAGAGATGTTGTCTGAGCCCTGACTATGTGAC 1421
Db 1658 CATTACTATAGAGAAAGCCGAGAGCTAATCATGTTCTGACGAGATTACCTGAC 1717
Qy 1422 AGAAAAGCATCAGCATGCTGAGATTAACT 1454
Db 1718 TAAAGAGCCAGGCGTGAGCTCGAGAGTGACT 1750

RESULT 14
US-09-110-618-3
Sequence 3, Application US/09110618
Patent No. 6090918
GENERAL INFORMATION:
APPLICANT: Parnet, Patricia et al.
TITLE OF INVENTION: Receptor Designated 2F1
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/110,618
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/604,333
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2619
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2830 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: mu2F1
FEATURE:
NAME/KEY: CDS
LOCATION: 381..1994
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 435..1991
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 381..434
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Best Local Similarity 54.2%; Pred. No. 4.4e-13;
Matches 148; Conservative 0; Mismatches 125; Indels 0; Gaps 0;
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Qy 1242 TCGGGAAGAAGAAATTTGTATTACTGACCCCTCGGAGTTTGAAGAAATTTGG 1301
Db 1538 TAAAGAGAGTATATCTTTCTGAGAGCTTACCCAGGCTCTGGAAGAAACAGTTGG 1597
Qy 1302 ATACAGCTGTGATCTTTGACGAGACAGTCTGCGGGGAATACAGTGAAGCAGT 1361
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Page 14

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Job time : 76 secs

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Query Match 3.5%; Score 73; DB 4; Length 2830;
Best Local Similarity 54.2%; Pred. NO. 4,4e-13;
Matches 148; Conservative 0; Mismatches 125; Indels 0; Gaps 0
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Copyright (c) 1993 - 2003 CompuGen Ltd.

Run on: April 30, 2003, 09:15:29 ; Search time 172 Seconds

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Maximum DB seq length: 20000000000

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- 14: /cgn2_6/ptodata/1/pub/pnna/US60_PUBCOMB.seq.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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2	1075.4	52.1	1077	9	US-10-215-211-5
3	1069.2	51.8	2733	9	US-09-935-868-27
4	287.4	13.9	287	10	US-09-864-761-32830
5	220	10.7	478	10	US-09-864-761-16315
6	151	7.3	2061	9	US-10-011-548-3
7	149	7.2	169	10	US-09-864-761-21077
8	144.4	6.8	2537	9	US-10-011-548-34
9	139.4	7.0	1737	9	US-10-011-548-1
c 10	113.6	5.5	443	10	US-09-880-107-3616
11	95	4.6	400	10	US-09-864-761-4326
12	89.6	4.3	1626	10	US-09-981-421-3
13	89.6	4.3	1626	12	US-10-157-447-1
14	88.6	4.3	1977	10	US-09-764-853-235
15	88.6	4.3	1991	9	US-10-011-548-19
16	73	3.5	2830	12	US-10-157-447-3
17	71.8	3.5	734	9	US-10-091-438-56
18	71.8	3.5	734	10	US-09-764-853-407
19	59.6	2.9	1404	9	US-10-011-548-7
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					Sequence 21077, Appl1
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					Sequence 1616, Appl1
					Sequence 4326, Appl1
					Sequence 3, Appl1
					Sequence 1, Appl1
					Sequence 235, Appl1
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					Sequence 56, Appl1
					Sequence 407, Appl1
					Sequence 7, Appl1

ALIGNMENTS

20	59.6	2.9	1797	9	US-09-731-449-3	Sequence 3, Appl
21	59.6	2.9	2314	9	US-10-011-548-9	Sequence 9, Appl
22	59.6	2.9	2681	9	US-10-212-287-6	Sequence 6, Appl
23	59.6	2.9	2681	10	US-09-581-421-1	Sequence 1, Appl
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25	59.2	2.9	616	9	US-09-764-668-358	Sequence 358, App
26	56.8	2.8	1689	10	US-09-775-046-12	Sequence 12, App
27	56.4	2.7	606	9	US-10-004-633-46	Sequence 42, Appl
28	56.4	2.7	1704	9	US-10-004-633-38	Sequence 38, Appl
29	56.4	2.7	4989	10	US-09-899-9804-3	Sequence 3, Appl
30	53.6	2.6	2058	10	US-09-899-9804-4	Sequence 4, Appl
31	50	2.4	1770	10	US-09-731-175-1	Sequence 1, Appl
32	50	2.4	4910	10	US-09-880-107-2312	Sequence 2312, Appl
33	49.6	2.4	1782	10	US-09-731-175-3	Sequence 3, Appl
34	49.4	2.4	1686	10	US-09-775-046-14	Sequence 14, Appl
35	43	2.1	482	9	US-10-011-548-5	Sequence 5, Appl
36	41.6	2.0	1833	9	US-10-011-548-13	Sequence 13, Appl
37	41.6	2.0	1845	9	US-10-212-287-1	Sequence 1, Appl
38	41.6	2.0	2259	9	US-10-011-548-15	Sequence 15, Appl
39	39.4	1.9	1357	9	US-10-215-211-1	Sequence 1, Appl
40	39.4	1.9	1357	9	US-10-199-209-1	Sequence 1, Appl
41	39.4	1.9	1357	10	US-09-854-162-1	Sequence 1, Appl
42	39.4	1.9	1357	10	US-09-921-667-7	Sequence 7, Appl
43	39.2	1.9	520	9	US-10-184-644-332	Sequence 332, App
44	39.2	1.9	520	10	US-10-184-634-332	Sequence 332, App
45	38.2	1.9	407	9	US-09-918-995-16653	Sequence 16653, A

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RESULT 1
US-10-215-211-3
: Sequence 3, Application US/10215211
: Publication NO. US20030049255A1
: GENERAL INFORMATION:
: APPLICANT: Sims, John E.
: APPLICANT: Smith, Dirk E.
: TITLE OF INVENTION: INTERLEUKIN-1 RECEPTORS IN THE TREATMENT OF DISEASES
: FILE REFERENCE: 3321-A
: CURRENT APPLICATION NUMBER: US/10/215,211
: CURRENT FILING DATE: 2002-08-07
: PRIOR APPLICATION NUMBER: US 60/310,789
: PRIOR FILING DATE: 2001-08-07
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 3
: LENGTH: 1713
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(1713)
: OTHER INFORMATION:
: US-10-215-211-3

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Query Match	Best Local Similarity	Matches 1515	Conservative	Score 1385.2	Pred. No. 0	Mismatches 173	Indels 6	Gaps 2
Qy	1	ATGACACTTCTGTGGTGTGTAGTAGAGTCTTCACTTTTATGGAATCTGCAAAAGTATGCC	60	67.1%				
Dy	1	ATGACACTTCTGTGGTGTGTAGTAGAGTCTTCACTTTTATGGAATCTGCAAAAGTATGCC	60					
Qy	61	TCAGAACCTTCGATGACTGGGGACTAGACACCATGAGGCCAAATCCAAAGTGTTTGAAGT	120					
Dy	61	TCAGAACCTTCGATGACTGGGGACTAGACACCATGAGGCCAAATCCAAAGTGTTTGAAGT	120					
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Dy	121	GAGCAGCTGCATCAAGATGGCCACTCTTTTGAACACTCTTGGAAATTCACAATACAGACACA	180					
Qy	181	GCCCAATCAGCTGAGCTTACTCTGATCTGTATATGCACTAGGACAGACCGGACCTTGAG	240					

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Db 241 GAGCCAAATTAATCTCCGCTCCCTGAGAACCGCAATTAGTAAGAGAAAGATGCTGTGG 300
Qy 301 TTCCGGCCACTCTCTCAAGACATGAGCAATCTACCTGCAATGTTAAAGAACTACA 360
Db 301 TTCCGGCCACTCTCTCAAGACATGAGCAATCTACCTGCAATGTTAAAGAACTACA 360
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RESULT 2
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; Sequence 5, Application US/10215211
; Publication No. US20030049255A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Dirk E.
; TITLE OF INVENTION: INTERLEUKIN-1 RECEPTORS IN THE TREATMENT OF DISEASES
; FILE REFERENCE: 3321-A
; CURRENT APPLICATION NUMBER: US/10/215,211
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US 60/310,789
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1077)
; OTHER INFORMATION:
US-10-215-211-5

Query Match 52.1%; Score 1075.4; DB 9; Length 1077;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1076; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy	1304	ACAAGCTGTGACTTTTGACCGAGACAGTGTGCTCGGGGGGAAATACAGTGAAGACGTTT	1361
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Qy	1364	TTGATTTCAATTCAGAGAGCAAGAAAGATGTGTGTCTGAGCCCTGTACTATGTGACAG	1421
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Qy	1424	AAAAGAGATACGACTGCTGAAGTTTAA	1452
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RESULT 7
US-09-864-761-21077
; Sequence 21077, Application US/09864761
; Patent No. US2002064763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.

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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIORITY APPLICATION NUMBER: US 60/180,312
PRIORITY FILING DATE: 2000-02-04
PRIORITY APPLICATION NUMBER: US 60/207,456
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: US 09/632,366
PRIORITY FILING DATE: 2000-08-03
PRIORITY APPLICATION NUMBER: GB 24263.6
PRIORITY FILING DATE: 2000-10-04
PRIORITY APPLICATION NUMBER: US 60/236,359
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: PCT/US01/00666
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00667
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00664
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00669
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00665
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00662
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00661
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00670
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: US 60/234,687
PRIORITY FILING DATE: 2000-09-21
PRIORITY APPLICATION NUMBER: US 09/608,408
PRIORITY FILING DATE: 2000-06-30
PRIORITY APPLICATION NUMBER: US 09/774,203
PRIORITY FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 21077
LENGTH: 169
TYPE: DNA
ORGANISM: Homo sapiens
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OTHER INFORMATION: NT HIT: AF167340.1, EVALUATE 1.00e-90
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US-09-864-761-21077

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OY 963 TACCTGTGAGATCTCAAGCGAGCTATCTGTCTATGCTAGAGTCCCAAGCGAGCT 1022
 DB 61 TACCTGTGAGATCTCAAGCGAGCTATCTGTCTATGCTAGAGTCCCAAGCGAGCT 120
 OY 1023 TGGCAAGACGACGAGCTGACGAGAG 1051
 DB 121 TGGCAAGACGACGAGCTGACGAGAG 149

RESULT 8

US-10-011-548-34
 ; Sequence 34, Application US/10011548
 ; Publication No. US2003005218A1
 ; GENERAL INFORMATION:

APPLICANT: Timans, Jacqueline C.
 Debets, Johannes Eduard Maria
 Antonius
 Sana, Theodore R.
 Bazan, J. Fernando
 Kastelein, Robert A.

TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and
 Methods

NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:

ADDRESSEE: DNA Research Institute
 STREET: 901 California Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA

ZIP: 94304-1104
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/011,548.
 FILING DATE: 22-Oct-2001
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/173,151
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 60/065,776
 FILING DATE: 17-Nov-1997

APPLICATION NUMBER: US 60/078,008
 FILING DATE: 12-Mar-1998

APPLICATION NUMBER: US 60/081,883
 FILING DATE: 15-Apr-1998

APPLICATION NUMBER: US 60/095,987
 FILING DATE: 10-Aug-1998

APPLICATION NUMBER: US 60/078,416
 FILING DATE: 18-Mar-1998

APPLICATION NUMBER: US 60/062,066
 FILING DATE: 15-Oct-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DX0767X

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 852-9196
 TELEFAX: (650) 496-1200

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 2537 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

MOLECULE TYPE: cDNA
 FEATURE:

NAME/KEY: CDS
 LOCATION: 1..2004
 SEQUENCE DESCRIPTION: SEQ ID NO: 34:

US-10-011-548-34

Query Match 7.0%; Score 144.4; DB 9; Length 2537;
 Best Local Similarity 46.2%; Pred. No. 7.9e-33;
 Matches 640; Conservative 0; Mismatches 701; Indels 45; Gaps 3;

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DB	88	GCTTATATACAGAAATTAATCTCCCTTGCCCAAGCTGAGCTGATGATGAGTAC	147
OY	214	TGGACTAGGACGAGCCGAGCTTGAAGAGCCAAATTAATCTCCGCTCCCGGAGAACCCG	273
DB	148	AAATTTCTGCTCTGAGAGCTTTGAAGAGCAATAGCTT-----TTAGCGAAGTATA	201
OY	274	ATTAGTAAGAGAAAGATGTGCTGTGTTCCGCGCCCACTCTCTCAATGACCTGGCAAC	333
DB	202	ATGAGCAAAAGAGAGACTCCATTGGTTCCGCGCAACATTCCTACAGAGCAGTGTCTC	261
OY	334	TATACCTGATGTTAAGAGACATATATGACAGAAAGTGCATTCCCTTGGAAATT	393
DB	262	TACGCTGTGATCAGAGAACTCCACTTAATGTAAGAAATGATTCATCTCAGTACAGTG	321
OY	394	GTTCAAAAGACAGCTGTTTCAATTCGCCCAATGAATCCAGTGCAATATGATATA	453
DB	322	GGTGAAATGACACTGAGACTCTGCTATATATCCAAAGATGAAATTTTGAAGAGCTGA	381
OY	454	GAATATGCAATTCAGAGATCACTGTCCAAATGATGATGATTTTCTTCCAGTGTG	513
DB	382	CTTACAAAGAGAGAAATTTATGACCGGTGATAGAGGATTTTCTACGCAACAGA	441
OY	514	AAACGACATATCACTTGTATGAGCGCTTATTAATAATACAAATTTAATATGTAAT	573
DB	442	GAACCTGAATCTTGTGTACAAAGAAATGACAGCAAAACATGAGGCGCAAGTATGTA	501
OY	574	CCCGAAGGTATGAATGATGATGATTTCTCATTTGCTTAATTTCAATATGAAATTAACA	633
DB	502	TTCAAAAGATATCTCTCTTATAGAGAGTCAAGAGATGACATTTGAAATTTATACC	561
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DB	562	TGTGAATTAATATAGAG-----GTTTGTGTAAGAAACTACTGAAATTA	609
OY	694	AAAGTATGAGCTCTCCAAATATGACAGTCCCTGCTGATCATCTTACCTATATGAT	753
DB	610	ACTGTTACAGCCCTCTGACTGATAGCCCAAGCTTTTGTATCTATGAGAAATGATA	669
OY	754	GTGCTATGAGAAAGAACAGAGAGAGTACATTTCCCTGTAAGGTATTTAGT	813
DB	670	CTGACATTCAGAGAGCCAGCTGGGTATCTGTCTAATCTAATCTGACAGACTTCTTT	729
OY	814	TTTGTATGATATTCGCAATGAGTTTGTGAGACATTTGAGAAATTAATGATGAC	873
DB	730	GGGTACAGCGAGATGATGATCTTTATTTATCTGATGAAAGAGAAATTTATTTGA	789
OY	874	ATCACTATTTATGATCAATTAACAAAGTATATGATATGTAACAGAGATGATAA	933
DB	790	GATCTGATGAAATATGAGTTGGAGAAAGTGCATTAAATTTTAAGAGAGATCTGGG	849
OY	934	AGAACTCAGATTTTGAAGATGAAAGTATCTTGTGAGATCTCAAGCGCATATGTC	993
DB	850	GAACGAGAGTTTCATTTCAATTAATTTGATCTGTGAGAAAGTGAATCTTGGAAAT	909
OY	994	TGTATGCTAAGAGTCCAAAGCGCAAGTTCCCAAGAGAGTGAAGAGAGAAAGT	1053
DB	910	TACTCTGTTATGTTGAAATGAAATGAGAGTGAACAGCCAGGCTTCTCTTATATAA	969
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DB	970	CGAGAGCTAATGATACAGTGAAGTCTGAGAGCTTGTGAGTATATCTTGTGCTT	1029

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us-10-061-727-1.rnpb

Page 8

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DB 1210 GAAATCTTACCTGATGATGCTTGAAGCAATTAAGATTAAGTTTATTAACCAAGATTA 1269
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QY 1387 AGGATGATTTGTTTCTGAGCCCTGACTATGTGACAGAAAGAGCATCAGATGCTGGAG 1446
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QY 1447 TTTTAA 1452
DB 1390 CTGGA 1395

RESULT 9
US-10-011-548-1
Sequence 1, Application US/10011548
Publication No. US2003005218A1
GENERAL INFORMATION:
APPLICANT: Tilmans, Jacqueline C.
Debets, Johannes Eduard Maria
Antonius
Sana, Theodore R.
Bazan, J. Fernando
Kastelein, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESS: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,548
FILING DATE: 22-OCT-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/173,151
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
APPLICATION NUMBER: US 60/062,066

FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-9196
TELEFAX: (650) 496-1200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1737 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: YES
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1737
FEATURE:
NAME/KEY: misc_feature
LOCATION: 342..343
OTHER INFORMATION: /note= "splice junction"
FEATURE:
NAME/KEY: misc_feature
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LOCATION: 756..757
OTHER INFORMATION: /note= "splice junction"
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OTHER INFORMATION: /note= "splice junction"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1177..1178
OTHER INFORMATION: /note= "splice junction"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1350..1351
OTHER INFORMATION: /note= "splice junction"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-011-548-1
Query Match 6.8%; Score 139.4; DB 9; Length 1737;
Best Local Similarity 47.8%; Pred. No. 2e-31;
Matches 678; Conservative 0; Mismatches 681; Indels 60; Gaps 7;
QY 64 GAACGTGGAGTACTGGGGATTAACACATGAGGCAAAATCCAGTGTGTAAGATAG 123
DB 70 GATGCTGATGATGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 126
QY 124 CCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 183
DB 127 CAGTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 186
QY 184 CATTCAGTGGCTTACTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 243
DB 187 CAGAGCACTGGGCTCAGGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 244 CCAATTAATTCCTCCGCTCCCGAGAACCCGATTAAGAGAGAGAGAGAGAGAGAGAGAG 303
DB 241 CCAATTAATTCCTCCGCTCCCGAGAACCCGATTAAGAGAGAGAGAGAGAGAGAGAGAG 294
QY 304 CGGCCACTCTCTCAATGACACTGACACTGATGATGATGATGATGATGATGATGATGATGAT 363
DB 295 CACTAGCTGAGGACAGAT 354

Qy 364 TGCAGAAAGTTCATTTCCCTTGAAGTGTTCACAAAGACAGCTGTTCAATTCCTCC 423
 Db 355 TGCATGAAGTGTCAATGCTTGTGACGTTGCAAGAAATGACAGCCGTGCTACAC 414
 Qy 424 ATGAACCTCCAGTGCATTAATCTGTATATGAAATATGCGATTGAGAGTCACTGTCCA 483
 Db 415 AACAGAGTCCGCTATTTAGAAAATCTGAAGTCACTAAAGAAAGAGATCTCTCTCCA 474
 Qy 484 AATGTATGATGATTTTCTTCCAGTCAAAACGAGTATCACTGTATATGAGCTGT 543
 Db 475 GACATGATGATCTTTAAAGTCCGATCAGAGCTGATGTTGTGTATATGAGATGC 534
 Qy 544 TATTAATAACAGATTTTATATATATATATATATATATATATATATATATATATAT 603
 Db 535 AAGCCAAAATGTGAGAAAGCATATATATATATATATATATATATATATATATATAT 594
 Qy 604 GCCTTATTTCAATATATGAAATTAACATGTTGTTATCATATTCAGAAAATGACGT 663
 Db 595 GTTCAAGAAAGATGAGAAATTAACATGTTGTTATATATATATATATATATATATAT 654
 Qy 664 AGGTTTCACTCAACAGAGCTGAGCTGTAAGTATAGTATAGTATAGTATAGTATAGT 723
 Db 655 AAGAGAACTGATTTGAAAGTTTACAGCTTATCTACAGACAAAGCTCCCAAGCATTG 714
 Qy 724 CCCCCTGATCCATTCACCTATATATATATATATATATATATATATATATATATATAT 783
 Db 715 TTCCCATGAGAAATCAGCAAGTGTATATAGATGTC-----CAGCTGGGTAAAGCT 765
 Qy 784 CTACTGATTTCCCTGACGGTCTATATTTAGTTTCTGATGATTTCTGCAATGAGTTTGG 843
 Db 766 CTGAACATCCCTCGCAAGATCTTCGAGTTCAAGAGAGTCTGGGCAATGATCTAC 825
 Qy 844 TGGACATTTGATGAGAAAAAAGCTGATGACATCATATGATGTCACATTAAGAAAGT 903
 Db 826 TGGATGAAAGAGAAAGTTTATATATATATATATATATATATATATATATATATAT 885
 Qy 904 ATTAAGTAT 963
 Db 886 AGGCTTCTCAAGAGATCTTGAAGAAAGAAAGTTGAATGACATCTTTGACTCA 945
 Qy 964 ACCTCTGAGATCTCAAGGAGCTATATGTTCTGATGATGATGATGATGATGATGATG 1023
 Db 946 GTTGTGAAAGTGAAGCTGAGAAATATATATATATATATATATATATATATATAT 999
 Qy 1024 GCCAAGAGAGAGTGAAGGAGAAAGTCCAGCTCCAGATATCAAGTGAAGTGGCT 1083
 Db 1000 CGAAGAGAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1059
 Qy 1084 TGTGTTTGAAGCAGAGTCTGATGATGATGATGATGATGATGATGATGATGATGATG 1143
 Db 1060 GGGGAGCTGGAGCAATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1119
 Qy 1144 TGGCTAGAGATGCTCTATTTTACCGGGCTCATTTTGAACAGATGAACATTTTGAAT 1203
 Db 1120 AACATTTGAATGATGCT 1179
 Qy 1204 GGAAGAGATGAT 1239
 Db 1180 AACAGAGAT 1239
 Qy 1240 ----AATGCGAAGAGAGAAATTTATATATATATATATATATATATATATATATAT 1296
 Db 1240 GACATCTCTGAG 1299
 Qy 1297 TTTGATATACAGCTGATCTTTGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1353
 Db 1300 TATGAT 1359
 Qy 1354 GAAAGAGTTTAT 1413
 Db 1360 GAAGATCTCAAGAT 1419

Qy 1414 TATGTACAGAAAGATCATGATGCTGAGTTTAA 1452
 Db 1420 TATATTTCTCAGAGCGAGATGAGTATTTTGAATCGAA 1458

RESULT 10

US-09-880-107-3616/c
 ; Sequence 3616, Application US/09880107
 ; Patent No. US20020142981A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Horne, Darci T.
 ; APPLICANT: Vockley, Joseph G.
 ; APPLICANT: Scherf, Iwe
 ; APPLICANT: Gene Logic, Inc.
 ; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
 ; FILE REFERENCE: 44921-5028-WO
 ; CURRENT APPLICATION NUMBER: US/09/880.107
 ; CURRENT FILING DATE: 2001-06-14
 ; PRIOR APPLICATION NUMBER: US 60/211,379
 ; PRIOR FILING DATE: 2000-06-14
 ; PRIOR APPLICATION NUMBER: US 60/237,054
 ; PRIOR FILING DATE: 2000-10-02
 ; NUMBER OF SEQ ID NOS: 3950
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3616
 ; LENGTH: 443
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 W85847
 ; NAME/KEY: unsure
 ; LOCATION: (1)-(443)
 ; OTHER INFORMATION: n = a or c or g or t
 ; US-09-880-107-3616

Query Match 5.5%; Score 113.6; DB 10; Length 443;
 Best Local Similarity 89.4%; Pred. No. 5.8e-24;
 Matches 144; Conservative 0; Mismatches 15; Indels 2; Gaps 2;

Qy 893 TTAAGGAAAGTATAGTCTATGATAGACAGAGATGAACAGAACTCAGATTTTGAAG-C 951
 Db 442 TTAAGGAAAGTATAGTCTATGATAGACAGAGATGAACAGAACTCAGATTTTGAAGC 383
 Qy 952 ATCAAGAAAGTATAGTCTGAGATCT-CAAGCGAGTATGCTGTCATGCTAGAGTGC 1010
 Db 382 ATCAAGAAAGTATAGTCTGAGATCTCAAGCGAGTATGCTGTCATGCTAGAGTGC 323
 Qy 1011 CAAGCGAGTATAGTCTGAGATCTCAAGCGAGTATGCTGTCATGCTAGAGTGC 1051
 Db 322 AAAGCGAGTATAGTCTGAGATCTCAAGCGAGTATGCTGTCATGCTAGAGTGC 282

RESULT 11

US-09-864-761-4326
 ; Sequence 4326, Application US/09864761
 ; Patent No. US20020048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharon G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wenheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL F
 ; FILE REFERENCE: Aecmika-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864.761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: GB 24263.6

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; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 4326
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; TYPE: DNA
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; FEATURE:
; OTHER INFORMATION: MAP TO AC008249.14
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1
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US-09-864-761-4326
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Query Match 4.6%; Score 95; DB 10; Length 400;
Best Local Similarity 100.0%; Pred. No. 2.5e-18;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Dy 366 GTTAACTCTGAGATCTCAAGCGCAGCTATGCTG 400

RESULT 12
US-09-981-421-3
; Sequence 3, Application US/09981421
; Patent No. US20020098185A1
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Mohler, Kendall M.
; APPLICANT: Born, Teresa L.
; TITLE OF INVENTION: METHODS FOR TREATING IL-18 MEDIATED DISORDERS
; FILE REFERENCE: 3086-A
; CURRENT APPLICATION NUMBER: US/09/981,421
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; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: US 60/241,408
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1626)
; OTHER INFORMATION:
US-09-981-421-3

Query Match 4.3%; Score 89.6; DB 10; Length 1626;
Best Local Similarity 46.3%; Pred. No. 2.9e-16;
Matches 391; Conservative 0; Mismatches 429; Indels 24; Gaps 2;
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Qy 604 GCCTTAATTCATTAATGAAGATTAACATGTTGTTACATATCCAGAAATGACGT 663
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Dy 583 CTATTTAATATCAACCAAACTTCAATATTAACATAGTGAAGATGCGATATATAGTT 642
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Qy 844 TGACACATTTGAGAAAAAACTGATGACATCATATTGATGATGATGATGATGATGAT 903
Dy 763 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 822
Qy 904 ATTAAGTATGATGAAGACAGAGATGAAGAACTCAGATTGAGCATCAAGAAATG 963
Dy 823 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 882
Qy 964 ACCTGAGATCTCAAGCGCAGCTATGCTGATGATGATGATGATGATGATGATGAT 1023
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; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 235

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Thu May 1 09:36:46 2003

us-10-061-727-1.rnpb

Page 12

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; LENGTH: 1977
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-853-235

Query Match
Best Local Similarity 52.8%; Score 88.6; DB 10; Length 1977;
Pred. No. 6.7e-16;
Matches 236; Conservative 0; Mismatches 184; Indels 27; Gaps 1;

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QY 1153 ATGCTCTATTATACCGGCTCATTTTGGAAACAGATGAACCATTTTACATGGAAGAG 1212
DB 509 ATCATCTCTTCAACAGATCATTTTGGAGCTGAAGAGCTGATGAGCATATAAGAT 568
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DB 689 AATTTGTTTATACCAAGTGAAGATTAATCCCACTGGAACATACATTAAGATGGA 748
QY 1366 GATTTCAATCAGAGAAAGAGAGATGTTGTTCTGAGCCCTGATCTATGTGACAGAA 1425
DB 749 AGATGTGTAGATCAAGCAAGCGGCTGATATGTGATGACCCCAATTAATGATTAAG 808
QY 1426 AAGAGATCAGACATGCTGAGTTTAA 1452
DB 809 AGGGGCTGAGCATCTTTGAGCTGAA 835

RESULT 15
US-10-011-548-19
; Sequence 19, Application US/10011548
; Publication No. US20030055218A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; Debets, Johannes Eduard Maria
; Antonius
; Sana, Theodore R.
; Bazan, J. Fernando
; Kastelein, Robert A.
; TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and
; Methods
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/011,548
; FILING DATE: 22-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: 09/173,151
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/065,776
; FILING DATE: 17-NOV-1997
; APPLICATION NUMBER: US 60/078,008
; FILING DATE: 12-MAR-1998
; APPLICATION NUMBER: US 60/081,883
; FILING DATE: 15-APR-1998
; APPLICATION NUMBER: US 60/095,987
; FILING DATE: 10-AUG-1998
; APPLICATION NUMBER: US 60/078,416
; FILING DATE: 18-MAR-1998
; APPLICATION NUMBER: US 60/062,066
; FILING DATE: 15-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0767X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 852-9196
; TELEFAX: (650) 496-1200
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1991 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1458
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-011-548-19

Query Match
Best Local Similarity 52.8%; Score 88.6; DB 9; Length 1991;
Pred. No. 6.7e-16;
Matches 236; Conservative 0; Mismatches 184; Indels 27; Gaps 1;

QY 1033 GCCAAGGTGAAGAGAAAGTCCAGCTCCAGATACACAGTGAAGTGGCTTGGTTT 1092
DB 403 GCCAGGGTCTCTCTTCAATAAACGAGCTAATGTACACAGTGAAGCTTGGAGGCCCTT 462
QY 1093 GGAGCCACAGTCCGTAGTGTGATTCATTTGTTTACATGTTTACAGTGGCTAGAG 1152
DB 463 GGTGCTATCTCTTGGCTTGTATGTGTGTGATCCATCTCAAGTGTACAAAGATGAA 522
QY 1153 ATGCTCTATTATACCGGCTCATTTTGGAAACAGATGAACCATTTTACATGGAAGAG 1212
DB 523 ATCATCTCTTCAACAGATCATTTTGGAGCTGAAGAGCTGATGAGCATATAAGAT 582
QY 1213 TATGATATTATATCTCT-----ATGCAAGGAATGCG 1245
DB 583 TATGATGCAATCTTATCATACCAAAAGTGAATCTGACCAAGTGAATCAAGAGCTGG 642
QY 1246 GAAGAGAAAGATTGTAATCTGACCCCTCGGAGTTTGGAGATGAATTTGGATAC 1305
DB 643 GAAGAGAAAGATTGTAATCTGAAATCTGATATGCTTGAAGAGCATTAATGATAT 702
QY 1306 AAGCTGTGATCTTTTACCGAGACAGCTGCTGGGGAAATACAGTGAAGAGATTTT 1365
DB 703 AAGTGTGTATACCAAGTGAAGATTAATCCCACTGGAACATACATTAAGATGGA 762
QY 1366 GATTTCAATCAGAGAAAGAGAGATGTTGTTCTGAGCCCTGATCTATGTGACAGAA 1425
DB 763 AGATGTGTAGATCAAGCAAGCGGCTGATATGTGATGACCCCAATTAATGATTAAG 822
QY 1426 AAGAGATCAGACATGCTGAGTTTAA 1452
DB 823 AGGGGCTGAGCATCTTTGAGCTGAA 849

Search completed: April 30, 2003, 10:47:51
Job time : 184 secs
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GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 30, 2003, 07:18:20; Search time 1999 Seconds
(without alignments)
16722.103 Million cell updates/sec

Title: US-10-061-727-1

Perfect score: 2064
Sequence: 1 atgacactctctgctgctc.....acgactttatccctataa 2064

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Indexed: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estropl:*
- 6: em_estro:*
- 7: em_estro:*
- 8: em_hic:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hic:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: gb_gss:*
- 18: em_gss_hum:*
- 19: em_gss_inv:*
- 20: em_gss_pln:*
- 21: em_gss_vrt:*
- 22: em_gss_fun:*
- 23: em_gss_mam:*
- 24: em_gss_mus:*
- 25: em_gss_other:*
- 26: em_gss_pro:*
- 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1039	50.3	1549	11	BC016141 Homo sapi
2	708.6	34.3	849	9	AL543511 AL543511
3	701.6	34.0	873	13	BI662501 BI662501
4	632.2	30.6	814	14	BQ006059 UI-H-E11-
5	601.2	29.1	880	13	BI330085 BI330085
6	513.8	24.9	923	9	AL544533 AL544533

7	511.8	24.8	596	10	AV656295
8	501	24.3	789	10	AV659167
9	500.4	24.2	756	9	AI303998
10	499.6	24.2	723	10	AW211290
11	490.8	23.8	910	12	BE892231
12	489	23.7	489	14	BI760155
13	486.4	23.6	580	13	BI346913
14	453	21.9	888	13	BI313184
15	413	20.0	652	10	BB625831
16	406.8	19.7	533	9	AA239486
17	405.8	19.7	598	9	AA237107
18	399.2	19.3	643	9	AA107505
19	396.8	19.2	676	10	BB626271
20	396.8	19.2	643	10	BB653335
21	390.8	18.9	616	10	AV661936
22	383.4	18.6	646	10	BB612046
23	382.2	18.5	396	14	T08277
24	381.8	18.5	637	10	BB623025
25	372	18.0	500	9	AA571281
26	356.4	17.3	885	12	BF237012
27	355.4	17.2	475	14	BQ561650
28	342.2	16.6	537	13	BI340158
29	341.8	16.6	567	14	BM751599
30	337	16.3	644	9	AA819412
31	325.8	15.8	545	10	BB633613
32	325.2	15.8	355	10	AV654169
33	277.6	13.4	426	14	T70863
34	275.6	13.4	570	14	H80590
35	275.2	13.3	392	10	AA427989
36	267	12.9	632	13	BI065068
37	254.4	12.3	586	12	BG711109
38	254.4	12.3	38	12	BG032519
39	249.8	12.1	850	13	BI872969
40	227.6	11.0	520	10	AI529899
41	224	10.9	305	10	AA485290
42	222.2	10.8	415	10	BB644209
43	213	10.3	547	10	BE013056
44	212.4	10.3	309	14	T85756
45	212.2	10.3	217	12	BF838851

ALIGNMENTS

RESULT 1	BC016141	1549 bp	mRNA	linear	HTC 24-OCT-2001
LOCUS	BC016141				
DEFINITION	Homo sapiens, interleukin 1 receptor accessory protein, clone IMAGE:3920152, mRNA.				
ACCESSION	BC016141				
VERSION	BC016141.1	GI:16359373			
KEYWORDS	HTC.				
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens				
REFERENCE	Strausberg, R.				
AUTHORS	Direct Submission				
TITLE	Submitted (22-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov				
COMMENT	Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC/DCPD/BTP CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E.B. Consortium (LNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bgsc.bc.ca Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,				

Thu May 1 09:36:47 2003

us-10-061-727-1.rst

Page 2

Susana Chato, Readman Chiu, Chris Fjell, Ruth Garland, Ran Guin, Setlicia Haito, Martin Krzyzinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeary, Steven Ness, Pawan Pandoh, Anna-Lisa Pridnu, Parvaneh Saeedi, Jacqueline Schein, Duane Smallus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Nastasja van den Bosch, Jill Wardy, George Yang, Scott Zyndredyn, Marco Marra.

Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.linl.gov>
Series: IRAP Plate: 15 Row: 1 Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 4504660
This clone has the following problem: frame shifted.

FEATURES	location/Qualifiers
source	1. .1549

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/organism="Homo sapiens"
/db_xref="locusID:3556"
/db_xref="taxon:9606"
/clone="IMAGE:3920152"
/tissue_type="Skin, melanot
/clone_id="NH MGC 72"
/lib_host="MD10B"
/notes="vector: pcmv-sports"
BASE COUNT      480 a      331 g      398 t
ORIGIN

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Query Match	50.3%	Score 1039	DB 11	Length 1549
Best Local Similarity	99.9%	Pred. No. 1.6e-297		
Matches 1050, Conservative	0	Mismatches 0	Indels 1	Gaps 1

Qy	1	ATGACACTTCTGTGGTGTGATGAGTCTCACTTTTAATGAATCCGCAAGATGATGCC	60
Db	206	ATGACACTTCTGTGGTGTGATGAGTCTCACTTTTAATGAATCCGCAAGATGATGCC	265
Qy	61	TCAGAACCGCTCGATGATCTGGGAGCTAGACAACAATGAGCAAAATCCAGTGTGAAGAT	120
Db	266	TCAGAACCGCTCGATGATCTGGGAGCTAGACAACAATGAGCAAAATCCAGTGTGAAGAT	325
Qy	121	GAGCAGCTGCCATCAACATGCGCACTCTTAAACACTCTTGAATTCACATACAGACA	180
Db	326	GAGCAGCTGCCATCAACATGCGCACTCTTAAACACTCTTGAATTCACATACAGACA	385
Qy	181	GCCCAATTCAGCTGGCCTTACTCTGATCTGTATTTGACATAGGCAAGACCGGACCTTGAG	240
Db	386	GCCCAATTCAGCTGGCCTTACTCTGATCTGTATTTGACATAGGCAAGACCGGACCTTGAG	445
Qy	241	GAGCCAAATTAACCTTCCGCTCCCGAGAACCGGCAATGATAGAGAGAAAGATGTCTGTGG	300
-/-	446	GAGCCAAATTAACCTTCCGCTCCCGAGAACCGGCAATGATAGAGAGAAAGATGTCTGTGG	505
Db	301	TTCCGGCCCACTCTTCTTCATATGACACTGGCAACTATACCTGCAATGTAAAGAACATACA	360
Qy	506	TTCCGGCCCACTCTTCTTCATATGACACTGGCAACTATACCTGCAATGTAAAGAACATACA	565
Db	361	TATTGCAAGCAAAAGTTGCAATTTCCCTTGGAAATGTGTCAAAAGACAGCTGTTCAATTC	422
Qy	566	TATTGCAAGCAAAAGTTGCAATTTCCCTTGGAAATGTGTCAAAAGACAGCTGTTCAATTC	622
Db	421	CCCAATGAACCTCCAGTGCATATAACTGTATATAGAAATATGSCATTCAGAGATCACTGT	480
Qy	626	CCCAATGAACCTCCAGTGCATATAACTGTATATAGAAATATGSCATTCAGAGATCACTGT	688
Db	481	CCCAATGTAGATGATATTTTCTTCCAGTGTCAACCGCATATCATCTGTGATATATGGGC	540
Qy	686	CCCAATGTAGATGATATTTTCTTCCAGTGTCAACCGCATATCATCTGTGATATATGGGC	745
Db	541	TGTTATATAAATAACGAATTTTATATATATATATATATATATATATATATATATATATAT	600
Qy	746	TGTTATATAAATAACGAATTTTATATATATATATATATATATATATATATATATATATAT	805
Db	601	ATTGCTTAATTTCAAAATATAGAAATTTACATGTGTTGTTACATATCCAGAAATATGA	660

D	b	806	ATGGCTTAATTTCAAATATATGAAATATACACATGTGTGTTTACTATATCCAGAAAATGGA	865
O	y	661	CGTACGTTTCATCTCCACGAGACCTCTGA CTGTAAAGGTAGAGCTCTCCAAAAATGCA	720
D	b	866	CGTAGTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGAGCTCTCCAAAAATGCA	925
O	y	721	GTCGCCCTGTGATCCATTCACTATATGATCATGTGTGCTATGAGAAAGAACGAGAGAG	780
D	b	926	GTGCCCTGTGATCCATTCACTPAATGATCATGTGTGCTATGAGAAAGAACGAGAGAG	985
O	y	781	GAGCTACTATTCCTGTGACGCTCTATTTTAGTTTCTGATGAGATTCTCGCAATAGATT	840
D	b	986	GAGCTACTATTCCTGTGACGCTCTATTTTAGTTTCTGATGAGATTCTCGCAATAGATT	1045
O	y	841	TGCTGACCATTTGATGGAAGAAAAACCTGATGACATCATATTTGATGTCACCATTAAGCA	900
D	b	1046	TGCTGACCATTTGATGGAAGAAAAACCTGATGACATCATATTTGATGTCACCATTAAGC-A	1104
O	y	901	AGTATPAGTCATPAGTAGAACAAGAGATGAAACAAGAACTCAGATTTTGAGCATCAAGAA	960
D	b	1105	AGTATPAGTCATPAGTAGAACAAGAGATGAAACAAGAACTCAGATTTTGAGCATCAAGAA	1164
O	y	961	GTTACTCTGAGGATCTCAAGGCGAGTATGTCTGTCATGCTAGAGAGTCCAAAGGCGAA	1020
D	b	1165	GTTACTCTGAGGATCTCAAGGCGAGTATGTCTGTCATGCTAGAGAGTCCAAAGGCGAA	1224
O	y	1021	GTTCGCAAGCAGCCAGGTGAGACAGAAAG	1051
D	b	1225	GTTCGCAAGCAGCCAGGTGAGACAGAAAG	1255

RESULT 2	AL543511	849 bp	mRNA	linear	EST 16-FEB-2001
LOCUS	AL543511				
DEFINITION	AL543511 LTI_NFL006_PL2 Homo sapiens cDNA clone CS001003YK15 5				
ACCESSION	AL543511				
VERSION	AL543511.1	GI:12875969			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Li, W.B., Gruber, C., Jessae, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	unpublished (2001)				
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqrete@genoscope.cns.fr, Web : www.genoscope.cns.fr.				

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FEATURES
SOURCE
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Location/Qualifiers
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/ld_xref="taxon:9606"
/clone="CSOD1003YK15"
/clone_lib="VTI NPL006 Pl.2"
/tissue_type="Placenta"
/notes="Vector: pCMVSPORT 6; Site 1: NotI; 1st
was primed with a NotI-oligo(dT) primer.
enriched, double-stranded cDNA was digested w
cloned into the Not I and Eco RV sites of the
vector. Library was normalized. Library was c
Life Technologies. Contact : Feng Liang Life
a division of Invitrogen 9800 Medical Center
Rockville, Maryland 20850, USA Fax : (1) 301
Email : fliang@lifestech.com URL :
http://lifelength.invitrogen.com"
BASE COUNT
232 a 206 c 185 g 224 t 2 others
Query Match 34.3%; Score 708.6; DB 9; Length 849
Best Local Similarity 99.4%; Pied. No. 36-199;

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Qy	987	CTATCTCTGTCATCTGTA - AGTCCAAAGCCGAG - TTGCCAAACACCTCAAGGTGAAG	1044
Db	720	CTATGTCGTGTCATCTGTAAGGATGCCAAAGTTTCCAAACACGACCAAGGTGAAG	779
Qy	1045	CAGAAAGTCCTCA	1056
Db	780	CAGAAAGGTACA	791

RESULT 4	
B006059/c	
LOCUS	B006059
DEFINITION	814 bp mRNA linear EST 26-MAR-2002
IMAGE:5845638 3'	UT-H-E11-ayz-f-07-0-U.s1 NCI CGAP_E11 Homo sapiens CDNA clone
IMAGE:5845638 3'	mRNA sequence.
ACCESSION	B006059

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euteleia; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 814)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.

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1. .814
/organism="Homo sapiens"
/db_xref="taxon.9606"
/clone_image="5845638"
/clone_id="NCI CGAP E11"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="RDH108 (Life Technologies)"
/notes="Organ: Left Pelvis; Vector: pT773-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoR I; Site_2: Not I
NCI CGAP E11 is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma. The library was
constructed according to Bonaldi, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT773-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
drr18 tail. The sequence tag for this library is
CGACTTCGAC."

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BASE COUNT	206 a	164 c	157 g	286 t	1 others
ORIGIN					

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Query Match          30.6%; Score 632.2; DB 14; Length 814;
Best Local Similarity 99.4%; Pred.No.17e-176;
Matches 634; Conservative 0; Mismatches 4; Indels 0; Gaps 0
QY 412 TTCATTCCCGCATGAACGCCAGGCGATAACTGTATATTAAGATATGCAATTCGAGG 471
|||||

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Db	814	TTCAATTC	CCCCCATGAAACTCC	CAGTGCATAACTG	TATATGAATATGCAATTCAGAGG	755
Oy	412	ATCACTGT	CCCAAAATGATGATG	GAATATTTCTTC	CAATGTCAAACGACATATCATCTGG	531
Db	754	ATCACTGT	GTCCAAAGTATGAGATG	AATTTTCTTC	CAAGTGTCAAAACGACATATCATCTGG	695
Oy	532	TATATGGCTG	TATATAAATA	CAGAAATTTTATAATG	TAAATCCCGAAGATATGAACTTG	591
Db	694	TATATGGCTG	TATATAAATA	CAGAAATTTTATAATG	TAAATCCCGAAGATATGAACTTG	635
Oy	592	AGTTTCCT	CATTTGCTTAATTTCA	ATAATGAAATTTAC	ATGTTGTATCATATTC	651
Db	634	AGTTTCCT	CATTTGCTTAATTTCA	ATAATGAAATTTAC	ATGTTGTATCATATTC	575
Oy	652	GAAATGGA	ACGATCCTTATCTCA	CCAGGACTG	ACGTAAAGATGATAGCTCTCCA	711
Db	574	GAAATGGA	ACGATCCTTATCTCA	CCAGGACTG	ACGTAAAGATGATAGCTCTCCA	515
Oy	712	AAAAATGCA	GTGCCCTCTGTGAT	CCATTCACCTTAATGAT	CATGTGCTATATGAAAGAA	771
Db	514	AAAAATGCA	GTGCCCTCTGTGAT	CCATTCACCTTAATGAT	CATGTGCTATATGAAAGAA	455
Oy	772	CCAGGAGAG	AGACTATCTATTC	CCCTGTACGGTCTATATTTA	GTGTTTCTGATGAGATTTCTGCC	831
Db	454	CCAGGAGAG	AGACTATCTATTC	CCCTGTACGGTCTATATTTA	GTGTTTCTGATGAGATTTCTGCC	395
Oy	832	AATGAGTTT	GCTGACCAATTG	ATGAAAAAAACCTG	ATGACATACATATGATGATGTCACC	891
Db	394	AATGAGTTT	GCTGACCAATTG	ATGAAAAAAACCTG	ATGACATACATATGATGATGTCACC	335
Oy	892	ATTAAACGA	AGATATATGATCAT	ATGTAGAAACAG	AGATGAAACAGAACTCAGATTTTGAGC	951
Db	334	ATTAAACGA	AGATATATGATCAT	ATGTAGAAACAG	AGATGAAACAGAACTCAGATTTTGAGC	275
Oy	952	ATCAAGAA	AGTTTACTCTGTAG	AGATCTCAAGCGAC	CTATGTCTGTATGCTATGAAAGTGC	1011
Db	274	ATCAAGAA	AGTTTACTCTGTAG	AGATCTCAAGCGAC	CTATGTCTGTATGCTATGAAAGTGC	215
Oy	1012	AAAGCGA	AGTTTCCAAAGC	ACGCAAGGTGAAAGC	AGAA 1049	
Db	214	AAAGCGA	AGTTTCCAAAGC	ACGCAAGGTGAAAGC	AGAA 177	

RESULT 5	
B1330085	
LOCUS	880 bp mRNA linear EST 30-JUL-2001
DEFINITION	B1330085 6029982187F1 NCI CGAP_L19 Mus musculus cDNA clone IMAGE:5135061 5',
ACCESSION	B1330085
VERSION	B1330085.1 GI:15014755
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eumaxyota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE	1 (bases 1 to 880)
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Contact: Robert Strausberg, Ph.D. Published (1999)

FEATURES
 source
 Tissue Procurement: Jeffrey B. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MSC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LIML at:
<http://image.liml.gov>
 Plate: L14M1131 row: n column: 22
 High quality sequence start: 3
 High quality sequence stop: 870.
 Location/Qualifiers
 1..880

/organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:5135061"
 /clone_lib="NCI_CGAP_Li9"
 /lab_host="DH10B (TI phage-resistant)"
 /note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.9 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP library."
 BASE COUNT 249 a 215 c 193 g 223 t
 ORIGIN

Query Match 29.1%; Score 601.2; DB 13; Length 880;
 Best Local Similarity 83.9%; Pred. No. 3.2e-167;
 Matches 715; Conservative 0; Mismatches 133; Indels 4; Gaps 3;

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137 AGTGGCCACTTTTGAACACTTCTTGAATCACTACGACGACCCCACTGAGCC 196
2 AGTGGCCACTTTTGAACACTTCTTGAATCACTACGACGACCCCACTGAGCC 61
197 TTACTCTGATCTGTATGATGACGACGACCCCACTGAGGACCAATTAATCTCC 256
62 TTACCTGATCTGTATGATGACGACGACCCCACTGAGGACCAATTAATCTCC 121
257 GCTCCGCGAGAACGCGATTAGTAAGAGAAAGATGCTGTGCTCCGACCACTCTCC 316
122 GCTCCGCGAGAACGCGATTAGTAAGAGAAAGATGCTGTGCTCCGACCACTCTCC 181
317 TCAATGACACTGGCACTATACCTGATGTAAAGAACATATATTCAGAGAAAGTTG 376
182 TCAATGACACTGGCACTATACCTGATGTAAAGAACATATATTCAGAGAAAGTTG 241
377 CATTTCCCTTGAAGATGTTCAAAAAGACGCTTTCAATTCCTCCATGAAGTCCGAG 436
242 CATTTCCCTTGAAGATGTTCAAAAAGACGCTTTCAATTCCTCCATGAAGTCCGAG 301
437 TGCATTAATCTGATATAGATATGACATTCAGAGATCACTTCCAAATGTAGATGAT 496
302 TGCATTAATCTGATATAGATATGACATTCAGAGATCACTTCCAAATGTAGATGAT 361
497 ATTTTCCTTCCAGTGTCAAAACCGACTATCACTGTATATGGCTGTATAAATAACA 556
362 ACTTTCCTTCCAGTGTCAAAACCGACTATCACTGTATATGGCTGTATAAATAACA 421
557 ATTTTATATATATATATATCCGAAAGATATGAATTCAGATTCCTCATTCCTTATTTCA 616
422 ACTTTCATATATATATATATCCGAAAGATATGAATTCAGATTCCTCATTCCTTATTTCA 481
617 ATTAATGAAATTAACATGATGTTGTACATATCCAGAAATGAGAGTTCATCTCA 676
482 ATTAATGAAATTAACATGATGTTGTACATATCCAGAAATGAGAGTTCATCTCA 541
677 CCAGGACTCTGACTGTAAAGATAGTAGGCTCTCAAAAATGAGAGTTCATCTCA 736
542 CCAGGACTCTGACTGTAAAGATAGTAGGCTCTCAAAAATGAGAGTTCATCTCA 600
737 ATTCACCTATATATATATGATGTTGTATGAGAAAGAACGAGAGAGTTCATCTCA 796
601 ATTCCTCAATATATATATGATGTTGTATGAGAAAGAACGAGAGAGTTCATCTCA 660
797 ATTAATGAAATTAACATGATGTTGTACATATCCAGAAATGAGAGTTCATCTCA 856
661 GCAAGATCTATATATATATGATGTTGTATGAGAAAGAACGAGAGAGTTCATCTCA 720
857 GAAAAAATCTGATATATATATG-ATGTCACATTAACGAAAGTATAGTCAATAGT 915
721 GAAAGAGCTGATATATATATG-ATGTCACATTAACGAAAGTATAGTCAATAGT 780
916 AGAAGAG-AGATGAAACAGAACTAGATTTTGAAGATCAAGAAAGTATCTGAGG 973
781 TTACCGGAGAAAGATGAAACAGAGACTCAGAAATTTGAGATCAAGAAAGTATCTGAGG 840

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QY 974 ATCTCAGCGCA 985
 DB 841 ATCTCAGCGCA 852

RESULT 6
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 LOCUS
 DEFINITION AL544533 LTI NPL006 PL2 Homo sapiens cDNA clone CS0D1021YH20 5
 prime, mRNA sequence.
 VERSION AL544533
 KEYWORDS AL544533.1 GI:12877013
 SOURCE EST.

ORGANISM human.

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 923)
 Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
 source 1..923
 Location/Qualifiers

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0D1021YH20"
 /clone_lib="LTI NPL006 PL2"
 /tissue_type="Placenta"

/note="Vector: pCMVSPORT 6; Site 1: NotI, 1st strand cDNA
 was primed with a NotI-oligo(dt) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed by
 Life Technologies. Contact : Feng Liang Life Technologies,
 a division of Invitrogen 9800 Medical Center drive
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"

BASE COUNT 226 a 99 c 323 g 218 t 57 others
 ORIGIN

Query Match 24.9%; Score 513.8; DB 9; Length 923;
 Best Local Similarity 86.7%; Pred. No. 3.7e-141;
 Matches 547; Conservative 32; Mismatches 49; Indels 3; Gaps 2;

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148 TTGGAACACTCTGTAATTAATCACTACGACGACCCCACTGAGCTGATCTGATC 207
294 TTGGAACACTCTGTAATTAATTAAGTAAGGASAGGAGATTAAGTGGGGTTAGKGTATG 353
208 TGTATTTGACATGACGAGACCGGACCTTGAAGACCAATTAATCTCCGCTCCGAG 267
354 TGTATTTGACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 413
268 AACCGATTAGTAAGAGAAAGATGCTGTGCTCCG--GCCACTCTCCCTCATATGACA 325
414 AAGGSAATTAATGATGAGGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 473
326 CTGGCAACTATATCCGCAATTAAGGACATCACTATATGAGCAAGATGATATTCCT 385
474 CTGGCAACTATATCCGCAATTAAGGACATCACTATATGAGGAGGAGGAGGAGGAGGAG 533
386 TGAAGTTGTTCAAAAAGACAGCTGTTCAATTTCCCAATGAACTCCAGATGATAAAC 445
534 TGAAGTTGTTCAAAAAGACAGCTGTTCAATTTCCCAATGAACTCCAGATGATAAAC 593
446 TGTATTAATTAATTAATGACATTCAGAGATCACTGTTCCAAATGATAGATATTTTCTT 505
594 TGTATTAATTAATTAATGACATTCAGAGATCACTGTTCCAAATGATAGATATTTTCTT 653

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QY 506 CCAAGTGTCAAAACCACTATCAGTGTATATGAGCTGTATATAAATGAGAAATTTTATA 565
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 DB 893 ATGATCATGTGTGTATATGAGAAACAGAG 923
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 SUIT 7
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 LOCUS AV656295 596 bp mRNA linear EST 16-JAN-2002
 DEFINITION AV656295 GLC Homo sapiens cDNA clone GLCEPH02 3', mRNA sequence.
 ACCESSION AV656295
 VERSION AV656295.1 GI:9877309
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 596)
 Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
 Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
 Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
 Hu,G., Gu,J., Chen,Z. and Han,Z.
 Insight into hepatocellular carcinogenesis at transcriptome level
 by comparing gene expression profiles of hepatocellular carcinoma
 with those of corresponding noncancerous liver
 Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
 21625106
 JOURNAL Contact: Zeguang Han
 MEDLINE Chinese National Human Genome Center at Shanghai
 COMMENT 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919(ex.45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.
 TITLES
 YTTRES Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="GLCEPH02"
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 /dev_stage="Adult"
 /lab_host="SOLR"
 /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
 XhoI"
 BASE COUNT 201 a 111 c 125 g 159 t
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 Best Local Similarity 99.6%; Pred. No. 1.1e-140;
 Matches 513; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 537 GGGCTGTAAATACAGAAATTTATATATGTAATACCGAAGCTATGAACTTGAAGTTT 596
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 DB 9 GGGCTGTAAATACAGAAATTTATATATGTAATACCGAAGCTATGAACTTGAAGTTT 68
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 QY 597 CCTCATTCCTTAATTTCAAAATATGAAATATACATGTGTGTATACATATCCAGAAA 656
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DB 69 CCTCATTCCTTAATTTCAAAATATGAAATTTACAGATGTGTATATATCCGAAA 128
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 QY 657 TGAAGTAAAGGTAGTAGGCTCTCCAAAATGAGTGGCCCTGTGATTCATTCACCTA 716
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 DB 129 TGAAGTAAAGGTAGTAGGCTCTCCAAAATGAGTGGCCCTGTGATTCATTCACCTA 188
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 QY 837 TGAAGTAAAGGTAGTAGGCTCTCCAAAATGAGTGGCCCTGTGATTCATTCACCTA 896
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 QY 957 TGAAGTAAAGGTAGTAGGCTCTCCAAAATGAGTGGCCCTGTGATTCATTCACCTA 1016
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 DB 429 TGAAGTAAAGGTAGTAGGCTCTCCAAAATGAGTGGCCCTGTGATTCATTCACCTA 488
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 QY 1017 TGAAGTAAAGGTAGTAGGCTCTCCAAAATGAGTGGCCCTGTGATTCATTCACCTA 1051
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 LOCUS AV659167 GLC Homo sapiens cDNA clone GLCFB08 3', mRNA sequence.
 DEFINITION AV659167
 ACCESSION AV659167
 VERSION AV659167.1 GI:9880181
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 789)
 Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
 Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
 Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
 Hu,G., Gu,J., Chen,Z. and Han,Z.
 Insight into hepatocellular carcinogenesis at transcriptome level
 by comparing gene expression profiles of hepatocellular carcinoma
 with those of corresponding noncancerous liver
 Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
 21625106
 JOURNAL Contact: Zeguang Han
 MEDLINE Chinese National Human Genome Center at Shanghai
 COMMENT 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919(ex.45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.
 TITLES
 YTTRES Location/Qualifiers
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 /db_xref="taxon:9606"
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 /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
 XhoI"
 BASE COUNT 268 a 140 c 162 g 210 t 9 others

ORIGIN

Query Match 24.3%; Score 501; DB 10; Length 769;
 Best Local Similarity 92.0%; Pred. No. 2.2e-137;
 Matches 512; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 537 GGGCTGTTAAATACAGAAATTTAATATGTAATACCGAAGTATGAAGTT 596
 Db 47 GGGCTGTTAAATACAGAAATTTAATATGTAATACCGAAGTATGAAGTT 106
 Qy 597 CCTGATGCTTAAATTTCAATATGAATTAACATGTTGTTTACATATCCAGAAA 656
 Db 107 CCTGATGCTTAAATTTCAATATGAATTAACATGTTGTTTACATATCCAGAAA 166
 Qy 657 TGGAC-GTACGTTTCACTCAGCAGACTCTGCTGAAAGTAGAGCTCCCAAAA 715
 Db 167 TGGACGTTTCACTCAGCAGACTCTGCTGAAAGTAGAGCTCCCAAAA 226
 Qy 716 ATGACAGTCCCTCTGATTCATTCATTAATGATGATGCTATGAGAAAGAACAG 775
 Db 227 ATGACAGTCCCTCTGATTCATTCATTAATGATGATGCTATGAGAAAGAACAG 286
 Qy 776 GAGAGAGCTACTCATTCCTCTGAGCGTCTATTTTATGTTTCTGATGATTCGCAATG 835
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 Qy 896 AGCAAAAGTAAAGTCACTAGTATGAGAAAGATGAAACCAAGACTGATTTGAGCATCA 955
 Db 407 AGCAAAAGTAAAGTCACTAGTATGAGAAAGATGAAACCAAGACTGATTTGAGCATCA 466
 Qy 956 AGAAAGTAACTCTGAGATCTCAAGCGCAGTATGTTCTGTCAATGATGAGAGTCCCAAG 1015
 Db 467 AGAAAGTAACTCTGAGATCTCAAGCGCAGTATGTTCTGTCAATGATGAGAGTCCCAAG 526
 Qy 1016 GGAAGTTGCCAAGCAGCAGCAAGTGAAGCAAG 1051
 Db 527 GGAAGTTGCCAAGCAGCAGCAAGTGAAGCAAG 562

RESULT 9
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LOCUS FINITION
 A1303998 ui63d12.y1 Sugano mouse liver mlia Mus musculus cDNA clone
 IMAGE:1887095 5' similar to gb:X85999 M.musculus mRNA for
 interleukin 1 receptor accessory (MOUSE);, mRNA sequence.

ACCESSION
 A1303998 A1303998.1 GI:3987748

KEYWORDS
 EST.

ORGANISM
 house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS
 1 (bases 1 to 756)
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubugue, T.,
 Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Scheinberg, K., Steppe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.

TITLE
 The Washu-HMI Mouse EST Project
 JOURNAL
 Unpublished (1996)
 COMMENT
 Contact: Maria M/Mouse EST Project
 Washu-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.wustl.edu
 This clone is available royalty-free through LML; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

MG1:971419
 Seq primer: custom primer used
 High quality sequence stop: 345.
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 /organism="Mus musculus"
 /strain="C57BL"
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 /clone="IMAGE:1887095"
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 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: liver; Vector: pME18S-FL3; Site 1: DraIII
 (CAGCTGCTG); Site 2: DraIII (CAGCAATGCTG); 1st strand cDNA
 was primed with an oligo(dT) primer
 [ATGAGGCTTTTATTTTATTTT]; double-stranded cDNA was
 ligated to a DraIII adaptor [TTTGGCTTCTGCTG], digested
 and cloned into distinct DraIII sites of the pME18S-FL3
 vector (5' site CAGCTGCTG, 3' site CAGCAATGCTG). XhoI should
 be used to isolate the cDNA insert. Size selection was
 performed to exclude fragments <1.5kb. Library
 constructed by Dr. Sumio Sugano (University of Tokyo
 Institute of Medical Science). Custom primers for
 sequencing: 5' end primer CTTGCTGCTTAAAGCTGCG and 3' end
 primer CGACCTGAGCTCGAGCA."

BASE COUNT 199 a 185 c 167 g 195 t 10 others
 ORIGIN
 Query Match 24.2%; Score 500.4; DB 9; Length 756;
 Best Local Similarity 82.0%; Pred. No. 3.2e-137;
 Matches 570; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

Qy 18 TGTAGTGAATCTCTTACTTTTATGAAATCTCGAAAGTATGCTCGAAAGCTCGCATGA 77
 Db 2 TTTGATGAGTCTGCTCTTCTATGAGATCTCGAAGTCAATGCTTCGAGGCTGTGATGA 61.
 Qy 78 CTGGGAGCTAGACACCATGAGGCAATCCAGTGTGAAAGTGAAGCTGAGCTGCAATCA 137
 Db 62 CTGGGAGCTAGACACCATGAGGCAATCCAGTGTGAAAGTGAAGCTGAGCTGCAATCA 121
 Qy 138 GTGCCACTCTTTGAAACCTTCTGAAATTAACAATCAACAGACAGACGCCATTCAGCTGCGCT 197
 Db 122 GTGCCACTCTTTGAAACCTTCTGAAATTAACAATCAACAGACAGACGCCATTCAGCTGCGCT 181
 Qy 198 TACTGTGATCTGATGATGAGCACTGAGGAGACCGGACCTTGAGAGACCAATTAATTCG 257
 Db 182 TACCTGATCTGATGATGAGCACTGAGGAGACCGGACCTTGAGAGACCAATTAATTCG 241
 Qy 258 CTTCCCGAGAACCCGATTAAGTGAAGAAATGTCGTGCTGCTGCTGCTGCTGCTGCTGCT 317
 Db 242 CTTCCCGAGAACCCGATTAAGTGAAGAAATGTCGTGCTGCTGCTGCTGCTGCTGCTGCT 301
 Qy 318 CATGACACTGAGCACTATACCTGATGATGAGAAACATCAATATTTGAGCAAAAGTTGC 377
 Db 302 CATGACACTGAGCACTATACCTGATGATGAGAAACATCAATATTTGAGCAAAAGTTGC 361
 Qy 378 ATTTCCCTTGAAGTTGTTCAAAAAGACGCTGTTCAATTCCTCCCATGAAGTCCAGT 437
 Db 362 ATTTCCCTTGAAGTTGTTCAAAAAGACGCTGTTCAATTCCTCCCATGAAGTCCAGT 421
 Qy 438 GCATAACGTATATATGATATGAGCACTTGAAGAGATCACTTGTCCAAATATATATGATGA 497
 Db 422 GCATAACGTATATATGATATGAGCACTTGAAGAGATCACTTGTCCAAATATATATGATGA 481
 Qy 498 TTTTCCCTTGAAGTTGTTCAAAAAGACGCTGTTCAATTCCTCCCATGAAGTCCAGT 557
 Db 482 CTTGCTTCAATGATGAGCACTTGAAGAGATCACTTGTCCAAATATATATGATGA 541
 Qy 558 TTTTAAATATGTAATACCGAAGTATGAAGTGAAGTTCCTCATTTCTTAATTTCAAA 617
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QY 618 TAAATGAAATTAACATGCTGTTTACATATCCAGAAATGACGTATTCATCTAC 677
DB 602 ATACGGATATACACATGTCGGTACATATCCGAAAGACAGCTCTCTTCACTCAC 661
QY 678 CAGACTCTGACTGTAAAGGTAGTAGCTCTCCAA 712
DB 662 CANGACTGTGACTGTAAATGTGTGAGCTACCAAA 696

RESULT 10
AM211290 723 bp mRNA linear EST 03-DEC-1999
LOCUS u079007.y1 NCI CGAP Mam3 Mus musculus cDNA clone IMAGE:2648725.5
DEFINITION similar to gb:X85999.M.musculus mRNA for interleukin 1 receptor
accessory (MOUSE);, mRNA sequence.
ACCESSION AM211290
VERSION AM211290.1 GI:6517238
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 723)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILMI at:
www.bio.liml.gov/db/ftp/image/image.html
MG1:1029177
Seq primer: -40RP from Gibco
High quality sequence stop: 427.
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Location/Qualifiers
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/note="Organ: mammary; Vector: pCMV-Sport6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies, Inc. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."

BASE COUNT 206 a 148 c 182 g 186 t 1 others
ORIGIN
Query Match 24.2%; Score 499.6; DB 10; Length 723;
Best Local Similarity 82.4%; Pred. No. 5.3e-137;
Matches 596; Conservative 0; Mismatches 125; Indels 2; Gaps 2;

QY 624 AATTAACACATGCTGTTTACATATCCAGAAATGACGTATTCATCTAC 663
DB 1 AATTAACACATGCTGTTTACATATCCAGAAATGACGTATTCATCTAC 660
QY 684 TGTGACTGTAAAGGTAGTAGCTCTCCAAATGACGTGCCCCGTGTATTCATTCAC 743
DB 61 TGTGACTGTAAAGGTAGTAGCTCTCCAAATGACGTGCCCCGTGTATTCAC 740
QY 744 TAAATGATCATGTGCTTATAGAAAGACGAGAGAGACTCATCTATTCCTGTACGT 803

DB 121 AATGACCGTGTGCTATAGAAAGAACAGAGAGAACTGTATTCCTCGAAGT 180
QY 804 CTAATTTAGTTTTGATGATATTCGCAATGAGTTGGTGAACCATGATGAGAAAAA 863
DB 181 CTAATTTAGTTTTGATGATATTCGCAATGAGTTGGTGAACCATGATGAGAAAAA 240
QY 864 ACCGTATGACATCACTATTTAGATGCCATTAACGAAATAGTACATAGACAGACA 923
DB 241 GCCTATGACATCACTATTTAGATGCCATTAACGAAATAGTACATAGACAGACA 300
QY 924 AGATGAAACAGAACTCAGATTTTGAACATCAAGAAAGTTACTCTGAGATCTCAAGCG 983
DB 301 AGATGAAACAGAACTCAGATTTTGAACATCAAGAAAGTTACTCTGAGATCTCAAGCG 360
QY 984 CAGCTATGCTGTGATGCTGATGAGTCCCAAGGCAAGTTGGCCAAAGCCCAAGGTGAA 1043
DB 361 CAACTATGCTGTGATGCTGATGAGTCCCAAGGCAAGTTGGCCCAAGGTGAA 420
QY 1044 GCAGAAAGTCCAGCTCCAAATACACAGTGGACCTGCTGTTTGGAGCCACAGT 1103
DB 421 ACAGAAAGTCCAGCTCCAAATACACAGTGGACCTGCTGTTTGGAGCCACAGT 480
QY 1104 CCTGCTAGTGTGATGCTGATGAGTCCCAAGGCAAGTTGGCCCAAGGTGAA 1163
DB 481 CTTTCTGATGATGCTGATGAGTCCCAAGGCAAGTTGGCCCAAGGTGAA 540
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DB 541 TTAACCGGCTCATTTTGGAGAGAAACCAATTTAGATGAGAAAGATATATTTA 600
QY 1224 TGTATCTTATGACATGATGAGTGGAGAAAGATTTTGAATTTACTGAC-CTCCGCTGAG 1282
DB 601 TGTATCTTATGACATGATGAGTGGAGAAAGATTTTGAATTTACTGAC-CTCCGCTGAG 660
QY 1283 TTTTGAAGATGATTTTGGATCAAGCTGTGATCTTTGACCGAGACAGTCTGCTGGGG 1342
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QY 1343 GAA 1345
DB 720 GAA 722

RESULT 11
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LOCUS 601435065F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3920152.5,
DEFINITION mRNA sequence.
ACCESSION BE892231
VERSION BE892231.1 GI:10352355
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 910)
NIH-MGC http://mgc.ncbi.nlm.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DRP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILMI at:
http://image.liml.gov
Plate: LHM9751 row: a column: 17
High quality sequence stop: 710.
FEATURES
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Location/Qualifiers
1..910
/organism="Homo sapiens"

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/lab host="DH10B (phage-resistant)"
/notes="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 2 kb. Library constructed by Life
Technologies."

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Query Match	23.8%	Score 490.8;	DB 12;	Length 910;
Best Local Similarity	93.8%;	Pred. No. 2.6e-134;		
Matches 576;	Conservative 0;	Mismatches 32;	Indels 6;	Gaps 6;

OY	1	ANGACACTCTGTGGGTGTAGTGAAGTCTCTACTTTTATAGGAATCTCGAAAGTATGCG	60
	183	ATGACACTTCTGTGGTGTAGTGAAGTCTCTACTTTTATAGGAATCTCGAAAGTATGCG	242
OY	61	TCGAAACGCTGCATGACTGCGGAGCTAGA CACCATGAGGCAATCCAAAGTGTGGAAGT	120
Db	243	TCGAAACGCTGCATGACTGCGGAGCTAGA CACCATGAGGCAATCCAAAGTGTGGAAGT	302
OY	121	GAGCCAGCTGCATCAAGTGGCCACTCTTTGAAACACTCTTTGAAATTCACATCAGACAA	180
Db	303	GAGCCAGCTGCATCAAGTGGCCACTCTTTGAAACACTCTTTGAAATTCACATCAGACAA	362
OY	181	GGCCATTGAGCTGGCCCTTACTGTGATCTGTATTTGGA CTGAGGAGGACCGGGACTTTGAG	240
Db	363	GGCCATTGAGCTGGCCCTTACTGTGATCTGTATTTGGA CTGAGGAGGACCGGGACTTTGAG	422
OY	241	GAGCAATTAACTTCGCGCTCCGCCGAAACCGCATTAATGTAAGGAGAAAGATGCTGTGG	300
Db	423	GAGCAATTAACTTCGCGCTCCGCCGAAACCGCATTAATGTAAGGAGAAAGATGCTGTGG	482
OY	301	TTCCGGCCCACTCTCCTCAATGACATGCGA ACTATACCTGATCTGTTAAGGAACACTACA	360
Db	483	TTCCGGCCCACTCTCCTCAATGACATGCGA ACTATACCTGATCTGTTAAGGAACACTACA	542
OY	361	TATTGACGAAAGTTGCAATTTCCCTTGGAGTGTGTCAAAAAGACAGCTGTTTC -AATTC	419
Db	543	TATTGACG -AAGTTGCAATTTCCCTTGGAGTGTGTCAAAAAGACAGCTGTTTC AATTC	601
OY	420	CCCCATGAAACTCCCACTGCATPAA -CTGTATATGAAATA -TGCAATTCAAGGATCACT	477
Db	602	CCCCATGAAACTCCCACTGCATPAACTGTATATGAAATAATGGCAATTCAAGGATCACT	661
OY	478	TGTCAAATGTAGATGATATATTTCCCTCAAGTGAACCAACTATCACTTGATATAG	537
Db	662	TGTCCAATGTAGATGATATATTTCCCTCAAGT -AAACCGACATCACTTGATATAG	720
OY	538	GGCTGTTATPAAATACAGAAATTTTATPAAATGTAATA CCGAAAGTATGAACCTGAATTC	597
Db	721	GGCTG -TATPAAATACGCACTTCAATATGTAATCCGAAAGTGAACCTGAGTTGCATGC	779
OY	598	CTCATTCCTTAAAT 611	
Db	780	CTTAAATGCACTTAT 793	

RESULT	12
BMT60155	
LOCUS	
DEFINITION	BMT60155 489 bp mRNA linear EST 04-MAR-2007 K-BST0040658 S2SNU668s1 Homo sapiens cDNA clone S2SNU668s1-14-A03 5', mRNA sequence.
ACCESSION	BMT60155
VERSION	BMT60155.1 GI:19089770
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
	Mammalia; Eutheria; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE	1. (bases 1 to 489)
AUTHORS	Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheng,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE	21C Frontier Korean EST Project 2001
JOURNAL	Unpublished (2002)
COMMENT	Contact: Kim YS

Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel.: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@gmail.kr
Plate: 14 Row: A Column: 03
High quality sequence, stop: 489.

FEATURES	Location/Qualifiers
source	1. .489

BASE COUNT
ORIGIN

158 a 90 c 97 g 144 t

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S2SNU66881-14-A03"
/clone_1b="S2SNU66881"
/sex="M"
/tissue_type="Ascites"
/cell_type="Epithelial"
/cell_line="SNU-668"
/lab_host="Top10F"
/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
Site 2: NotI. The poly (A)+ RNA was decapped with tobacco
acid pyrophosphatase (TAP) and ligated with DNA-RNA linker
including EcoRI site by treatment of T4 RNA ligase. The
first strand cDNA was synthesized from oligo dT-selected
mRNA by priming with dT-tailed vector. The dT-tailed
vector was adjusted to have about 60nt. The cDNA vector
was circularized with E. coli DNA ligase after digestion
of EcoRI which site is also included in vector. An RNA
strand converted to a DNA strand by Okayama-Berg method.
The obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
After analyzing and sequencing about 2,000 ~ 3,000
colonies in original cDNA library, the abundant cDNAs were
selected and amplified by PCR reaction using vector region
primer including T7 promoter as 5' primer and N(dT)14 as
3' primer. The PCR products were used as template for
synthesis of biotinylated single stranded RNA by in vitro
transcription reaction. The synthesized RNA probes were
hybridized with antisense single stranded cDNAs prepared
from original library and incubated with avidin-gel.
After removing DNA-RNA hybrids by centrifuge, the
subtracted cDNA libraries were constructed by
transformation of the remaining DNA into competent cells E
coli Top10F with electroporation method."

[illegible]

Thu May 1 09:36:47 2003

us-10-061-727-1.rst

Page 10

OY	707	CTCCAAAAATCAGTGCCTCCCTGATCATTCACCTTAAGATCATGAGCTAATGAGA	766
Db	244	CTCCAAAAATCAGTGCCTCCCTGATCATTCACCTTAATATCATGAGCTAATGAGA	300
OY	767	AAGAAACAGAGAGAGAGCTACTCATTCCTCTGACGGTCTAATTTAGTTTCTGATGATT	826
Db	301	AAGAAACAGAGAGAGAGCTACTCATTCCTCTGACGGTCTAATTTAGTTTCTGATGATT	360
OY	827	CTGGACATGAGGTTTGTGTGACCATTTGATGAAAAAACCTGATGACATTAATGATG	886
Db	361	CTGGACATGAGGTTTGTGTGACCATTTGATGAAAAAACCTGATGACATTAATGATG	420
OY	887	TCACCATTTAACGAAGTATTAAGTCAATAGTAGAGAACGAAGATGAAAACAAGACTCAGATT	946
Db	421	TCACCATTTAACGAAGTATTAAGTCAATAGTAGAGAACGAAGATGAAAACAAGACTCAGATT	480
OY	947	TGAGCATCA	955
Db	481	TGAGCATCA	489

SULT 13	
LOCUS	B1346913 580 bp mRNA linear EST 30-JUL-2001
DEFINITION	376288 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION	B1346913
VERSION	B1346913.1 GI:15040211
KEYWORDS	
SOURCE	EST.
PIG.	

ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
1 (bases 1 to 580)
REFERENCE
Fahnenkrug, S. C., Prekling, B. A., Rohrer, G. A., Smith, T. P. L., Casas, F.,
AUTHORS

TITLE
JOURNAL
COMMENT

Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.N.
and Keele, J.W.
Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel.: 402 762 4366
Fax: 402 762 4390
Email: smthue@mail.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mismatch 18
and -mismatch 12 options.

```

PCR primers
FORWARD: AGGAACAGCTATGACCCAT
BACKWARD: GTTTCCTCAGTACGACG
Plate: 130 row: 1 column: 3
Seq primer: ATTGAGGACACTATGAC.

FEATURES
    source            1..580

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BASE COUNT
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/clone_id="MARC 2P1G"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."

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Query Match      23.6%   Score 486.4   DB 13   Length 580;
Best Local Similarity 91.8%   Pred. No. 3.9e-133;
Matches 538; Conservative 0; Mismatches 41; Indels 7; Gaps 2;

0Y  924  AGATGAACCAACTCAGATTGAGCATCAAGGTAAGTTACTCTGAGATCTCAAGC 983
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Db	2	AGATGAGCAAGGACCTGACCTTTTGAGATCAAG- AAGTAACTGCTGAGATCTCAAGG	60
Oy	984	CAGCTATCTCTGTCATGCTAGAGTCCCAAGGCGAAGTTGCCAAGCAAGCTGAA	1043
Db	61	CAACTATCTCTGTCATGCTAGAGTCCCAAGGCGAAGTTGACAGACCGGCGCAAGTGA	120
Oy	1044	GCAGAAATGCGACGCTCCAAATATACACAGTGGAACTGGCTTGCGTTTGGAGCCACAGT	1103
Db	121	AACAGAA-----ACTCCCAATATCACAGTGGAACTGGCAATGCGTTTGGAGCCACAGT	174
Oy	1104	CTGTCTAGTGGNGATTCCTCATTTGTTGTTTACCAAGTTTACTGGCGTACAGATGCTCTATT	1163
Db	175	CTGTGCTGATGATGATCTTCATTTGTTGTTTACCAATGTTTACTGGCTGAGATGCTCTCTT	234
Oy	1164	TTACCGGCGCTCATTTTGGAAACAGATGAACCATTTTAGATGAAAGAGTATGATATTTA	1223
Db	235	TTATCGGCGCTCATTTTGGAAACAGATGAACCATTTTAGATGAAAGAGTATGATATTTA	294
Oy	1224	TGTATCTTATGCAAGAAATGCGGAAAGAAAGAAATTTGTATTACTGACCTTCCTGGAGT	1283
Db	295	TGTATCTTATGCAAGAAATGCGGAAAGAAAGAAATTTGTATTACTGACCTTCCTGGAGT	354
Oy	1284	TTTGGAGAAATGAATTTGGATACAGCTGTGTGATCTTTGACCGGACACAGTCTGGCGGGGG	1343
Db	355	CTTGGAGAAATGAATTTGGATACAGCTGTGTGATCTTTGACCGGACACAGTCTGGCGGGGG	414
Oy	1344	AAATACAGTGGAGCAGTTTGTGATTTCAATTCAGAGAGCAGAAAGATGATTTGTGTCT	1403
Db	415	AAATACAGTGGAGCAGTTTGTGATTTCAATTCAGAGAGCAGAAAGATGATTTGTGTCT	474
Oy	1404	GAGCCCTGACTATGTGACAGAAAGAGCATCAGCATGCTGGAGTTTAACTGGGTGCAT	1463
Db	475	GAGCCCAAGACTATGTGACAGAAAGAGCATCAGCATGCTGGAGTTTAACTGGGTGCAT	534
Oy	1464	GTCGCAGAACTCCATTGCGACCAAGCTCATTTGTTGGTGAATGATACCGT	1509
Db	535	GTCGCAGAACTCCATTGCGACCAAGCTCATTTGTTGGTGAATGATACCGT	580

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RESULT 14  

LOCUS      B1331848  

DEFINITION B1331848          888 bp   mRNA    linear   EST 30-JUL-2001  

            602982528F1 NCI_CGAP_l19 Mus musculus cDNA clone IMAGE:5135287 5',  

ACCESSION  B1331848  

VERSION     B1331848  

KEYWORDS    GI::15016505  

SOURCE      EST.  

ORGANISM    house mouse.  

             Mus musculus  

REFERENCE   Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  

AUTHORS     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  

TITLE       1 (bases 1 to 888)  

JOURNAL     NIH-MGC http://mgc.nci.nih.gov/  

COMMENT     National Institutes of Health, Mammalian Gene Collection (MGC)  

            Unpublished (1999)  

            Contact: Robert Strausberg, Ph.D.  

            Email: cgabs@remail.nih.gov  

            Tissue Procurement: Jeffrey E. Green, M.D.  

            CDNA Library Preparation: Life Technologies, Inc.  

            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  

            DNA Sequencing by: Incyte Genomics, Inc.  

            Clone distribution: MGC clone distribution information can be  

            found through the I.M.A.G.E. Consortium/LNLT at:  

            http://image.lnl.gov  

            plate: LAMM1332 row: h column: 08  

            High quality sequence stop: 802.  

            Location/Qualifiers  

              1..888  

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                /strain="FVB/N"  

                /db_xref="taxon:10090"  

                /clone="IMAGE:5135287"  

                /clone_1ib="NCI CGAP l19"

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Query Match 20.0%; Score 413; DB 10; Length 652;
 Best Local Similarity 87.3%; Pred. No. 3.2e-111;
 Matches 452; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

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Oy 1 ATGACACTTCGTGAGTGTGTGATGAGTCTCACTTTATGGAATCCCTGCAAAAGTATGCC 60
Db 133 ATGGAGCTTCGTGAGTGTGTGATGAGTCTCTCTCTATGGAATCCCTGCAAGTCAATGCT 192
Oy 61 TCAGAAAGCTGCGATGATCTGAGGAGCTAGACACCATGAGCAATCCAAAGTGTGAAGAT 120
Db 193 TCGAGCGCTGTGATGATCTGAGGAGCTAGATACATGAGCAATCCAAAGTGTGAAGAT 252
Oy 121 GAGCGAGCTGCGATGATCTGAGGAGCTAGACACCATGAGCAATCCAAAGTGTGAAGAT 180
Db 253 GAGCGAGCTGAGATGATGAGGAGCTAGACACCATGAGCAATCCAAAGTGTGAAGAT 312
Oy 181 GCCCATTCAGCTGAGCTTACTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 240
Db 313 GCCCATTCCTCTGAGCTTACTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 372
Oy 241 GAGCCATTTAATCTTCGCTCTCCGAGAAACCGCATTTAGTGAAGAAAGATGCTGAG 300
Db 373 GAGCCATTTAATCTTCGCTCTCCGAGAAATCGATGATGAGAAAGATGCTGAG 432
Oy 301 TTCCGCGCCCACTCTCTCATATGACACTGCAACTATATCTGATGTTAAGAACTATCA 360
Db 433 TTCCGCGCCCACTCTCTCATATGACAGGCGCAATTAACCTGATGTTAAGAACTATCA 492
Oy 361 TATTCAGCAAGTGTGATTTCCCTTGAAGTGTTCAAAAGACAGCTGTTCAATTCC 420
Db 493 TACTGCAAGAAAGTGTGATTTCCCTTGAAGTGTTCAAAAGACAGCTGTTCAATTCT 552
Oy 421 CCATGAAACTCCAGTGTATTAACCTGTATATAGATATGCAATTCAGAGATCACTTGT 480
Db 553 GCCATGAAATCCAGTGTCAAGATGTATATGAAATGCAATTCAGATTCATAGATCATGT 612
Oy 481 CCAATGTAGATGATATTTTCTTCAGTCAAAACC 518
Db 613 TCAATGTAGAGGATACTTCTTCAGTCAAAACC 650
    
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Search completed: April 30, 2003, 09:40:11
 Job time : 2012 secs

[illegible]

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FT      /note= "Immunogenic epitope"
FT      365..411
FT      /note= "Immunogenic epitope"
FT      Region
FT      339..375
FT      /note= "Immunogenic epitope"
FT      401..431
FT      /note= "Immunogenic epitope"
FT      Region
FT      411..511
FT      /note= "Immunogenic epitope"
FT      501..517
FT      /note= "Immunogenic epitope"
FT      545..563
FT      /note= "Immunogenic epitope"
FT      Region
FT      US6280955-B1.
FT      28-AUG-2001.
FT      16-DEC-1997; 97US-0991944.
FT      16-DEC-1997; 97US-0991944.
FT      16-DEC-1997; 97US-0991944.
FT      (TUL- ) TULARIK INC.
FT      Cao Z;
FT      WPI: 2001-595441/67.
FT      N-PSDB: AAS15608.
FT      Isolated polypeptide designated interleukin receptor accessory
FT      polypeptide is useful for regulating cell function - accessory
FT      Claim 1; Fig 1; 21pp; English.
XX      This sequence represents the human interleukin-1 receptor accessory
XX      protein (IL-1Racp) of the invention. The interleukin receptor
XX      accessory protein (IL-1Racp) and its modulators (agonists/antagonists)
XX      are useful for regulating cell function. Transient expression of either
XX      IL-1RI or IL-1Racp alone does not result in ligand-independent induction
XX      of an NF-kappaB-dependent luciferase reporter gene in 293 cells, however
XX      coexpression of both proteins resulted in a 20-fold increase in
XX      activation of NF-kappaB activity to a level comparable to that induced
XX      by IL-1. These data suggest that aggregation of IL-1RI and IL-1Racp as
XX      a result of protein overexpression can elicit a signaling pathway
XX      leading to NF-kappaB activation. Modulating signal transduction
XX      involving NF-kappaB in a cell may be achieved by modulating the activity
XX      of IL-1Racp using binding agents such as agonists and antagonists.
XX      Hybridisation probes to the cDNA sequence can be used to identify wild-
XX      type and mutant IL-1Racp alleles in clinical and laboratory
XX      samples. Mutant alleles are used to generate allele-specific
XX      oligonucleotide (ASO) probes for high-throughput clinical diagnoses
XX      of diseases or disorders with an inflammatory response. In
XX      therapy, therapeutic IL-1Racp nucleic acids are used to modulate
XX      cellular expression or intracellular concentration or availability of
XX      active IL-1Racp. This invention also comprises a method of screening for
XX      an agent that modulates the interaction of an interleukin receptor
XX      accessory polypeptide (IL-1Racp) to a binding target.
XX      Sequence 570 AA;
XX      Query Match 70.5%; Score 2586; DB 22; Length 570;
XX      Best Local Similarity 85.3%; Pred No. 1.4e-212;
XX      Matches 488; Conservative 35; Mismatches 37; Indels 12; Gaps 4;

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DB      121 YCSKVAFLPVLVQKSCFNSPKMLPVHKLVIEXGIQIRICPNVDGFFSPSVKTLITWNG 180
DB      181 CYKIQNFNNVIBGNMISLALISNNGYTCVYTPENGRTFHLTRLLTVKVSPPKNA 240
DB      181 CYKIQNFNNVIBGNMISLALISNNGYTCVYTPENGRTFHLTRLLTVKVSPPKNA 240
DB      241 VPPVHSPNDHVYKEPEBELLPCTVYFSEFLMSRNMWMTTJGKRPDDITDVINE 300
DB      241 VPPVHSPNDHVYKEPEBELLPCTVYFSEFLMSRNMWMTTJGKRPDDITDVINE 300
DB      301 SISHSRTDETRTQILSIKVTSEDLKRSYGVASAKAEVAKAKVOKVAPARTVEL 360
DB      301 SISHSRTDETRTQILSIKVTSEDLKRSYGVASAKAEVAKAKVOKVAPARTVEL 360
DB      361 ACGFGATVLLVYVIVVYVWLEWVLFYRAHGTDETLIDGKEXDIYVSARNAEEEF 420
DB      361 ACGFGATVLLVYVIVVYVWLEWVLFYRAHGTDETLIDGKEXDIYVSARNAEEEF 420
DB      421 VLLTLRGVLENERGYKLCIFDRDSLPGCNTVEAVDFIORSRMIVYLSDDYVTEKISIM 480
DB      421 VLLTLRGVLENERGYKLCIFDRDSLPGCNTVEAVDFIORSRMIVYLSDDYVTEKISIM 480
DB      481 LEPKLGWMCNLSIATK---LIVEXRPLEHPHGLQKES---VSPVSMGKSKHSG 533
DB      481 LEPKLGWMCNLSIATK---LIVEXRPLEHPHGLQKES---VSPVSMGKSKHSG 533
DB      534 SKFWKALRLALPLRLSLASGSGNESCSSQSDI 565
DB      536 GRFWKQLQVAMPVKKSPRSSDDEGLSYSSL 567
XX      RESULT 2
XX      ID AAE16590 standard; Protein; 570 AA.
XX      AAE16590;
XX      09-APR-2002 (first entry)
XX      Human interleukin-1 receptor DNAX designation 3 (IL-1RD3) protein.
XX      Human; morphogenesis; immune system; interleukin-1 DNAX designation 3;
XX      IL-1RD3 protein; therapy; immunological disorder.
XX      Homo sapiens.
XX      US6326472-B1.
XX      04-DEC-2001.
XX      14-OCT-1998; 98US-0173151.
XX      15-OCT-1997; 97US-062066P.
XX      17-NOV-1997; 97US-065776P.
XX      12-MAR-1998; 98US-078008P.
XX      18-MAR-1998; 98US-078416P.
XX      15-APR-1998; 98US-081833P.
XX      10-AUG-1998; 98US-095987P.
XX      (SCHE ) SCHERING CORP.
XX      Timans JC, Debets JEMA, Sana TR, Bazan JF, Kastelein RA;
XX      WPI: 2002-121110/16.
XX      Antibody fragments which specifically bind to primate interleukin 1
XX      receptor-like molecules are useful to treat conditions associated with
XX      abnormal expression of the receptor or its ligand, particularly
XX      immunological disorders
XX      Disclosure; Column 51-54; 102pp; English.

```

CC The present invention relates to compositions and methods for affecting
 CC mammalian physiology such as morphogenesis of immune system function.
 CC The invention particularly relates to nucleic acids, proteins and
 CC antibodies which regulate development and/or the immune system. The
 CC invention also relates to antibody fragments which specifically bind
 CC to antigenic fragments of a primate interleukin (IL)-1 receptor like
 CC molecules such as IL-1 receptor DNAx designation (IL-1R α). The antibody
 CC fragments of the invention are useful to treat conditions exhibiting
 CC abnormal expression of the receptors or their ligands which typically
 CC will be immunological disorders. The present sequence is human IL-1R α
 CC protein.

CC
 XX
 SQ Sequence 570 AA;

Query Match 70.5%; Score 2586; DB 23; Length 570;
 Best Local Similarity 85.3%; Pred. No. 1.4e-212;

Matches 488; Conservative 35; Mismatches 37; Indels 12; Gaps 4;

```

1 MTLWCVSLVYFGILQSDASERCDWGLDTRQIQVFEDEPARIKCPLEHFLKENVST 60
1 MTLWCVSLVYFGILQSDASERCDWGLDTRQIQVFEDEPARIKCPLEHFLKENVST 60
61 AHSAGTLTIWYTRQDRLEBPINFLPENNRSKEKQVLMFRPTLNDTGNNTCMRLNTT 120
61 AHSAGTLTIWYTRQDRLEBPINFLPENNRSKEKQVLMFRPTLNDTGNNTCMRLNTT 120
121 YCSKVAFPLEVVOQSCFNSPMKLPVHKLYIEYGIQRTCPNDVGYPSSVAPRTITWYG 180
121 YCSKVAFPLEVVOQSCFNSPMKLPVHKLYIEYGIQRTCPNDVGYPSSVAPRTITWYG 180
181 CYKIONFNNVIEPEGNNISFLIALISNNGNYTCVVTYPENGRTFHLTRTLTVKVGSPKNA 240
181 CYKIONFNNVIEPEGNNISFLIALISNNGNYTCVVTYPENGRTFHLTRTLTVKVGSPKNA 240
241 VPPVHSPNDHVYVEKEPEEELIPICTVYFSPMDSRNEVMTIDGKDDITITVTINE 300
241 VPPVHSPNDHVYVEKEPEEELIPICTVYFSPMDSRNEVMTIDGKDDITITVTINE 300
301 SISHRTBETFTQTLISIKKTSSEDKRSYVCHABSAKEVAKAAVKQKVPARTVTEL 360
301 SISHRTBETFTQTLISIKKTSSEDKRSYVCHABSAKEVAKAAVKQKVPARTVTEL 360
361 ACSPGATVLLVYLIVVYVYVLEWLPFRAHGTDETLIDGKEVYIYVSARNAESEEF 420
361 ACSPGATVLLVYLIVVYVYVLEWLPFRAHGTDETLIDGKEVYIYVSARNAESEEF 420
421 VLLTRAGVLENEFGYKLCIFDRDSLPGGNTVAVPDPIORSRMIVLSPDYVTEKSISM 480
421 VLLTRAGVLENEFGYKLCIFDRDSLPGGNTVAVPDPIORSRMIVLSPDYVTEKSISM 480
481 LEFKIGWMCQNSIATK---LIVVERPLRLEHHPGILQLES---VSFVSKGSEKSHSG 533
481 LEFKIGWMCQNSIATK---LIVVERPLRLEHHPGILQLES---VSFVSKGSEKSHSG 533
534 SKFWKALRLALPLRSLASAGNNESSQSDI 565
534 SKFWKALRLALPLRSLASAGNNESSQSDI 565
536 GRPKQLQVAMFVKKSPRRSSDDEGLSTYSL 567
536 GRPKQLQVAMFVKKSPRRSSDDEGLSTYSL 567

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RESULT 3
 ID AAU09978 standard; Protein; 550 AA.
 AAU09978;
 AAU09978;

21-MAY-2002 (first entry)

Human IL-1R α CP protein deletion mutant delta C1.

IL-1R α CP; human; interleukin-1 receptor accessory protein; NF-kappaB;
 IL-1; IL-1R1; mutant; delta C1; inflammatory response.

OS Homo sapiens.

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XX US6280955-B1.
PN 28-AUG-2001.
XX 16-DEC-1997; 97US-0991944.
XX 16-DEC-1997; 97US-0991944.
XX (TULIA-) TULARIK INC.
XX Cao Z;
XX WPI; 2001-595441/67.
XX N-PESDB; AAS15608.
PT Isolated polypeptide designated interleukin receptor accessory
PT polypeptide is useful for regulating cell function
Disclousure; Page - 21pp; English.
CC This sequence represents the human interleukin-1 receptor accessory
CC protein (IL-1R $\alpha$ ) mutant delta C1 of the invention. This mutant
CC was used to define domains of the IL-1R $\alpha$  protein that have the
CC ability to activate NF-kappaB expression. The interleukin receptor
CC accessory protein (IL-1R $\alpha$ ) and its modulators (agonists/antagonists)
CC are useful for regulating cell function. Transient expression of either
CC IL-1R $\alpha$  or IL-1R $\alpha$  alone does not result in ligand-independent induction
CC of an NF-kappaB-dependent luciferase reporter gene in 293 cells, however
CC coexpression of both proteins resulted in a 20-fold increase in
CC activation of NF-kappaB activity to a level comparable to that induced
CC by IL-1. These data suggest that aggregation of IL-1R1 and IL-1R $\alpha$  as
CC a result of protein overexpression can elicit a signaling pathway
CC leading to NF-kappaB activation. Modulating signal transduction
CC involving NF-kappaB in a cell may be achieved by modulating the activity
CC of IL-1R $\alpha$  using binding agents such as agonists and antagonists.
CC Hybridisation probes to the cDNA sequence can be used to identify wild-
CC type and mutant IL-1R $\alpha$  alleles in clinical and laboratory
CC samples. Mutant alleles are used to generate allele-specific
CC oligonucleotide (ASO) probes for high-throughput clinical diagnoses
CC of diseases or disorders with an inflammatory response. In
CC therapy, therapeutic IL-1R $\alpha$  nucleic acids are used to modulate
CC cellular expression or intracellular concentration or availability of
CC active IL-1R $\alpha$ . This invention also comprises a method of screening for
CC an agent that modulates the interaction of an interleukin receptor
CC accessory polypeptide (IL-1R $\alpha$ ) to a binding target.
CC Note: The present sequence is not included in the
CC specification but was created from the human IL-1R  $\alpha$ CP sequence
CC appearing as AAU09966 and the information given in table 1 of the
CC specification.
SQ Sequence 550 AA;

```

Query Match 70.3%; Score 2580; DB 22; Length 550;
 Best Local Similarity 87.4%; Pred. No. 4.4e-212;

Matches 484; Conservative 33; Mismatches 25; Indels 12; Gaps 4;

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1 MTLWCVSLVYFGILQSDASERCDWGLDTRQIQVFEDEPARIKCPLEHFLKENVST 60
1 MTLWCVSLVYFGILQSDASERCDWGLDTRQIQVFEDEPARIKCPLEHFLKENVST 60
61 AHSAGTLTIWYTRQDRLEBPINFLPENNRSKEKQVLMFRPTLNDTGNNTCMRLNTT 120
61 AHSAGTLTIWYTRQDRLEBPINFLPENNRSKEKQVLMFRPTLNDTGNNTCMRLNTT 120
121 YCSKVAFPLEVVOQSCFNSPMKLPVHKLYIEYGIQRTCPNDVGYPSSVAPRTITWYG 180
121 YCSKVAFPLEVVOQSCFNSPMKLPVHKLYIEYGIQRTCPNDVGYPSSVAPRTITWYG 180
181 CYKIONFNNVIEPEGNNISFLIALISNNGNYTCVVTYPENGRTFHLTRTLTVKVGSPKNA 240
181 CYKIONFNNVIEPEGNNISFLIALISNNGNYTCVVTYPENGRTFHLTRTLTVKVGSPKNA 240

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QY 241 VPPVHSFNDHVVYKEKGESEELIPCTVYFSFLMDSRNEVWMTIDGKKPDDITIDVTINE 300
DB 241 VPPVHSFNDHVVYKEKGESEELIPCTVYFSFLMDSRNEVWMTIDGKKPDDITIDVTINE 300
QY 301 SISHSRTEDETRQIILSIKVTSEDLKRSYVCHARSAGKGEVAAKAVKQVAPARYVEL 360
DB 301 SISHSRTEDETRQIILSIKVTSEDLKRSYVCHARSAGKGEVAAKAVKQVAPARYVEL 360
QY 361 ACGRGATVLLVLLIIVVHYVYMLEMVLFRYAHFGTDETTIDGKEYDLYVSARNAEEREF 420
DB 361 ACGRGATVLLVLLIIVVHYVYMLEMVLFRYAHFGTDETTIDGKEYDLYVSARNAEEREF 420
QY 421 VLLTRGVLENEFGYKLCIFDRDSLPGCNTVEAVDFIORSRMIVLSPDYTEKISIM 480
DB 421 VLLTRGVLENEFGYKLCIFDRDSLPGCNTVEAVDFIORSRMIVLSPDYTEKISIM 480
QY 481 LEFRLGYMCONSIAATK---LIIVYRPLEHPHPIQLKES---VSFVSWKGEKSHSG 533
DB 481 LEKAGL---ENNASRGNINVLIVYKAVKETK--VKEIKRAKTVLTVIKWGEKSKYPO 535
QY 534 SKWKALRLALPLR 547
DB 536 GRFWKQLQVAMPVK 549

RESULT 4
ID AAM01911 standard; Protein; 570 AA.
AC AAM01911;
DT 14-OCT-1996 (first entry)
XX
XX Human interleukin-1 receptor accessory protein.
XX
XX Interleukin-1 receptor accessory protein; IL-1 antagonist;
XX inflammation; therapy; antiinflammatory; antibody;
XX rheumatoid arthritis; inflammatory bowel disease; septic shock;
XX transplant rejection; psoriasis; asthma; type 1 diabetes;
XX cancer; leukaemia.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX Peptide 1..20
XX Protein /label= Sig_peptide
XX Protein 21..570
XX Protein /label= Mat_protein
XX Domain 21..359
XX Domain /label= Extracellular_domain
XX Domain 360..383
XX Domain /label= Transmembrane_domain
XX Domain 384..570
XX Domain /label= Cytoplasmic_tail

MO9623067-A1.
XX
XX 01-AUG-1996.
XX
XX 17-JAN-1996; 96MO-EP00181.
XX
XX 23-JAN-1995; 95US-0376268.
XX
XX (HOF) HOFMANN LA ROCHE & CO AG F.
XX
XX Chizzone RA, Ju GM;
XX
XX WPI, 1996-362691/36.
XX
XX N-PSDB; AAT32026.
XX
XX Isolated interleukin-1 receptor accessory protein - used to develop
XX prods. to treat or prevent inflammatory or immunological activities
XX of interleukin-1

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XX
XX Claim 4; Page 74-75; 115p; English.
PS
XX Human interleukin-1 receptor accessory protein (IL-1R ACP) (AAM01911)
CC is a protein that inhibits the ability of IL-1 to bind to, or
CC otherwise activate, the IL-1R, esp. the type 1, IL-1R. It can be
CC obtd. in pure, recombinant form using a cDNA clone (AAT32026) obtd.
CC from YT cells. A soluble form (AAM01912) of human IL-1R ACP has also
CC been produced. The protein is partic. useful in preventing the
CC inflammatory or immunological activities of IL-1, esp. for the
CC treatment of rheumatoid arthritis, inflammatory bowel disease,
CC septic shock, transplant rejection, psoriasis, asthma, type 1
CC diabetes or acute and chronic myelogenous leukaemia.
XX
XX Sequence 570 AA:
SQ
Query Match 70.3%; Score 2580; DB 17; Length 570;
Best Local Similarity 85.6%; Pred. No. 4,7e-212;
Matches 487; Conservative 31; Mismatches 45; Indels 6; Gaps 3;

QY 1 MTLIMCVSLYFYGILOSASERCDMDGIDTMROIQVFEDEPARICPLFEHLKFNYST 60
DB 1 MTLIMCVSLYFYGILOSASERCDMDGIDTMROIQVFEDEPARICPLFEHLKFNYST 60
QY 61 AHSAGLTLIWMYTRDRLDEEPINFLPENRISKEDVLMFRPTLNDIGNYTCMLRNTT 120
DB 61 AHSAGLTLIWMYTRDRLDEEPINFLPENRISKEDVLMFRPTLNDIGNYTCMLRNTT 120
QY 121 YCSKVAEPLEVVQKSCFNSPMKLPHKLYIEYGIQITCPNVNGYFPSSVKEPTIYWG 180
DB 121 YCSKVAEPLEVVQKSCFNSPMKLPHKLYIEYGIQITCPNVNGYFPSSVKEPTIYWG 180
QY 181 CYKIQNPNVNIPEGMLSPFIALISNNNGNTCVVTPENGRTHLTRTLVKKVGSFKNA 240
DB 181 CYKIQNPNVNIPEGMLSPFIALISNNNGNTCVVTPENGRTHLTRTLVKKVGSFKNA 240
QY 241 VPPVHSFNDHVVYKEKGESEELIPCTVYFSFLMDSRNEVWMTIDGKKPDDITIDVTINE 300
DB 241 VPPVHSFNDHVVYKEKGESEELIPCTVYFSFLMDSRNEVWMTIDGKKPDDITIDVTINE 300
QY 301 SISHSRTEDETRQIILSIKVTSEDLKRSYVCHARSAGKGEVAAKAVKQVAPARYVEL 360
DB 301 SISHSRTEDETRQIILSIKVTSEDLKRSYVCHARSAGKGEVAAKAVKQVAPARYVEL 360
QY 361 ACGRGATVLLVLLIIVVHYVYMLEMVLFRYAHFGTDETTIDGKEYDLYVSARNAEEREF 420
DB 361 ACGRGATVLLVLLIIVVHYVYMLEMVLFRYAHFGTDETTIDGKEYDLYVSARNAEEREF 420
QY 421 VLLTRGVLENEFGYKLCIFDRDSLPGCNTVEAVDFIORSRMIVLSPDYTEKISIM 480
DB 421 VLLTRGVLENEFGYKLCIFDRDSLPGCNTVEAVDFIORSRMIVLSPDYTEKISIM 480
QY 481 LEFRLGYMCONSIAATK---LIIVYRPLEHPHPIQLKES---VSFVSWKGEKSHSGKF 536
DB 481 LEKAGLENNKSGRGNINVLIVYKAVKETK--VKEIKRAKTVLTVIKWGEKSKYPOGRF 538
QY 537 WKALRLALPLRLSASAGNESCSOSDI 565
DB 539 WKQLQVAMPVKSPRRSSSDQGLSYSSL 567

RESULT 5
ID AAM09979 standard; Protein; 540 AA.
AC AAM09979;
DT 21-MAY-2002 (first entry)
XX
XX Human IL-1R ACP protein deletion mutant delta C2.
XX
XX IL-1R ACP; human; interleukin-1 receptor accessory protein; NF-kappaB;
XX IL-1; IL-1RI; mutant; mutein; delta C2; inflammatory response.

```

QY 181 CYKJONENNVIPEGMNTSLIALISNNNGNTCVWTPYENGNTFHLTRILTIVKVVGSPKNA 240
|||||

CC This sentence represents the human interleukin-1 receptor accessory
CC protein (IL-1RAcP) mutant delta C3 of the invention. This mutant
CC was used to define domains of the IL-1RAcP protein that have the
CC ability to activate NF-kappaB expression. The interleukin receptor
CC accessory protein (IL-1RAcP) and its modulators (agonists/antagonists)
CC are useful for regulating cell function. Transient expression of either
CC IL-1RI or IL-1RAcP alone does not result in ligand-independent induction
CC of an NF-kappaB-dependent luciferase reporter gene in 293 cells, however
CC coexpression of both proteins resulted in a 20-fold increase in
CC activation of NF-kappaB activity to a level comparable to that induced
CC by IL-1. These data suggest that aggregation of IL-1RI and IL-1RAcP as

CC a result of protein overexpression can elicit a signaling pathway
 CC leading to NF-kappaB activation. Modulating signal transduction
 CC involving NF-kappaB in a cell may be achieved by modulating the activity
 CC of IL-1Racp using binding agents such as agonists and antagonists.
 CC Hybridization probes to the cDNA sequence can be used to identify wild-
 CC type and mutant IL-1Racp alleles in clinical and laboratory
 CC samples. Mutant alleles are used to generate allele-specific
 CC oligonucleotide (ASO) probes for high-throughput clinical diagnoses
 CC of diseases or disorders with an inflammatory response. In
 CC therapy, therapeutic IL-1Racp nucleic acids are used to modulate
 CC cellular expression or intracellular concentration or availability of
 CC active IL-1Racp. This invention also comprises a method of screening for
 CC an agent that modulates the interaction of an interleukin receptor
 CC accessory polypeptide (IL-1Racp) to a binding target.
 CC Note: The present sequence is not included in the
 CC specification but was created from the human IL-1R ACP sequence
 CC appearing as AAU09966 and the information given in table 1 of the
 CC specification.

XX Sequence 530 AA;

Query Match 68.9%; Score 2527; DB 22; Length 530;
 Best Local Similarity 89.0%; Pred. No. 1.5e-207;
 Matches 476; Conservative 26; Mismatches 21; Indels 12; Gaps 4;

QY 1 MTLLMVCVSLFYGILOSASERCDMDGLTMRQIOVEDEPARIKPLFEHFLKFNYSY 60
 DB 1 MTLLMVCVSLFYGILOSASERCDMDGLTMRQIOVEDEPARIKPLFEHFLKFNYSY 60
 QY 61 AHSAGLTLIWMTRQDDLEPINFRLPENRISKEKOVLMFRPLTNDTGYTCLMANTT 120
 DB 61 AHSAGLTLIWMTRQDDLEPINFRLPENRISKEKOVLMFRPLTNDTGYTCLMANTT 120
 QY 121 YCSKVAPELLEVQKDSGFNSPMKLPVHKLTYEIGIORTCPNVGVPSSVKTITWYMG 180
 DB 121 YCSKVAPELLEVQKDSGFNSPMKLPVHKLTYEIGIORTCPNVGVPSSVKTITWYMG 180
 QY 181 CYKIQNFNNVPEGMNLSFLIALISNNNGNTCVVTPENGRTFHLTRTLVKKVGSFKNA 240
 DB 181 CYKIQNFNNVPEGMNLSFLIALISNNNGNTCVVTPENGRTFHLTRTLVKKVGSFKNA 240
 QY 241 VPPYIHSNDVHYEKEGEBELIPTCYVFSFLMSDRNEVMTIDGKKPDITIDVTINE 300
 DB 241 VPPYIHSNDVHYEKEGEBELIPTCYVFSFLMSDRNEVMTIDGKKPDITIDVTINE 300
 QY 301 SISHRTDETRTQILSIKVTSEDLKRSYVCHASAKGEVAKAKVQKVPARYVEL 360
 DB 301 SISHRTDETRTQILSIKVTSEDLKRSYVCHASAKGEVAKAKVQKVPARYVEL 360
 QY 361 ACGGATATLVVILVYHYVWLEVLFYRAHFGTDETLIDGKDYDVYSARNAAREEP 420
 DB 361 ACGGATATLVVILVYHYVWLEVLFYRAHFGTDETLIDGKDYDVYSARNAAREEP 420
 QY 421 VLLTRAGVLENEFGYKLCIFPRDSLPGNTVEAVDFIQRSRMIVLSPPDYTEKISIM 480
 DB 421 VLLTRAGVLENEFGYKLCIFPRDSLPGNTVEAVDFIQRSRMIVLSPPDYTEKISIM 480
 QY 481 LEFKLVNCONSIAK---LIVVERPLEHPHGGIOLKES---VSFVSKGEG 528
 DB 481 LEFKLVNCONSIAK---LIVVERPLEHPHGGIOLKES---VSFVSKGEG 528
 QY 481 LELKAGL---ENMASRGNINVLIVQKAVKETK--VKELKRAKATVLIVIKWKGK 530
 DB 481 LELKAGL---ENMASRGNINVLIVQKAVKETK--VKELKRAKATVLIVIKWKGK 530

RESULT 7

ID AAU09973 standard; Protein, 559 AA.

XX AAU09973;

XX 21-MAY-2002 (first entry)

XX Human IL-1R ACP protein deletion mutant delta N1.

XX IL-1R ACP; human; interleukin-1 receptor accessory protein; NF-kappaB;

KW IL-1; IL-1RI; mutant; mutein; delta N1; inflammatory response.
 XX Homo sapiens.
 OS US6280955-B1.
 XX 28-AUG-2001.
 PD 16-DEC-1997; 97US-0991944.
 PF 16-DEC-1997; 97US-0991944.
 PR 16-DEC-1997; 97US-0991944.
 XX (TULAR-) TULARIK INC.
 PA Cao Z;
 PI WPI; 2001-595441/67.
 DR N-PSDB; AAS15608.
 XX Isolated polypeptide designated interleukin receptor accessory
 PT polypeptide is useful for regulating cell function
 PS Disclosure; Page - ; 21pp; English.

CC This sequence represents the human interleukin-1 receptor accessory
 CC protein (IL-1Racp) mutant delta N1 of the invention. This mutant
 CC was used to define domains of the IL-1Racp protein that have the
 CC ability to activate NF-kappaB expression. The interleukin receptor
 CC accessory protein (IL-1Racp) and its modulators (agonists/antagonists)
 CC are useful for regulating cell function. Transient expression of either
 CC IL-1RI or IL-1Racp alone does not result in ligand-independent induction
 CC of an NF-kappaB-dependent luciferase reporter gene in 293 cells, however
 CC coexpression of both proteins resulted in a 20-fold increase in
 CC activation of NF-kappaB activity to a level comparable to that induced
 CC by IL-1. These data suggest that aggregation of IL-1RI and IL-1Racp as
 CC a result of protein overexpression can elicit a signaling pathway
 CC leading to NF-kappaB activation. Modulating signal transduction
 CC involving NF-kappaB in a cell may be achieved by modulating the activity
 CC of IL-1Racp using binding agents such as agonists and antagonists.
 CC Hybridization probes to the cDNA sequence can be used to identify wild-
 CC type and mutant IL-1Racp alleles in clinical and laboratory
 CC samples. Mutant alleles are used to generate allele-specific
 CC oligonucleotide (ASO) probes for high-throughput clinical diagnoses
 CC of diseases or disorders with an inflammatory response. In
 CC therapy, therapeutic IL-1Racp nucleic acids are used to modulate
 CC cellular expression or intracellular concentration or availability of
 CC active IL-1Racp. This invention also comprises a method of screening for
 CC an agent that modulates the interaction of an interleukin receptor
 CC accessory polypeptide (IL-1Racp) to a binding target.
 CC Note: The present sequence is not included in the
 CC specification but was created from the human IL-1R ACP sequence
 CC appearing as AAU09966 and the information given in table 1 of the
 CC specification.

XX Sequence 559 AA;

Query Match 68.8%; Score 2525; DB 22; Length 559;
 Best Local Similarity 85.0%; Pred. No. 2.4e-207;
 Matches 477; Conservative 35; Mismatches 37; Indels 12; Gaps 4;

QY 12 FYGILOSASERCDMDGLTMRQIOVEDEPARIKPLFEHFLKFNYSYAHSAGLTLIY 71
 DB 1 FYGILOSASERCDMDGLTMRQIOVEDEPARIKPLFEHFLKFNYSYAHSAGLTLIY 71
 QY 72 WTRQDRLEEPINFRLPENRISKEKOVLMFRPLTNDTGYTCLMANTTCSKVAPELV 131
 DB 72 WTRQDRLEEPINFRLPENRISKEKOVLMFRPLTNDTGYTCLMANTTCSKVAPELV 131
 QY 132 VQKDSGFNSPMKLPVHKLTYEIGIORTCPNVGVPSSVKTITWYMGCKYONFNNVI 191
 DB 132 VQKDSGFNSPMKLPVHKLTYEIGIORTCPNVGVPSSVKTITWYMGCKYONFNNVI 191
 QY 192 PEGNLSFLIALISNNNGNTCVVTPENGRTFHLTRTLVKKVGSFKNAVPPYIHSNDH 251
 DB 192 PEGNLSFLIALISNNNGNTCVVTPENGRTFHLTRTLVKKVGSFKNAVPPYIHSNDH 251


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DB 181 PEGANISFLIALISNNGNVCTVTPENGRTFHLRLTLTKVVGSPGNAVPVISHSPNDH 240
QY 252 VYVEKERGSELLPCTVYFSFLMDSRNEVWMTIDGKKPDITIDVTINESISRTEDT 311
DB 241 VYVEKERGSELLPCTVYFSFLMDSRNEVWMTIDGKKPDITIDVTINESISRTEDT 300
QY 312 RQOILSIRKVTSEDLKRSYVCHARSAGKGEVAKAKAVKQKVPARYVELACGFGATVLLV 371
DB 301 RQOILSIRKVTSEDLKRSYVCHARSAGKGEVAKAKAVKQKVPARYVELACGFGATVLLV 360
QY 372 VILIVVHYVWLEMLVFLYRAHFGTDETTIDGKEYDIYVSAYARNAEERFVLLTLRGYLEN 431
DB 361 VILIVVHYVWLEMLVFLYRAHFGTDETTIDGKEYDIYVSAYARNAEERFVLLTLRGYLEN 420
QY 432 ERFYKLCIFDRDSLPGQIVTDETLISFLQKSRLLVLSPNVYLQGTALLETLAGL--E 477
DB 421 ERFYKLCIFDRDSLPGQIVTDETLISFLQKSRLLVLSPNVYLQGTALLETLAGL--E 477
QY 492 SIATK----LIVVEYRPLEHPHPIQLQKES---VSFVWKGKSKSKHSGKFWNALRLAL 544
DB 478 NMASRGNINIVLYQYKAVKETR--VKELKRAKTVLVTVIKKSKSKYPOGRFHWKQLQVAM 535
QY 545 PLRSLTASSGWNSSCSSQSDI 565
DB 536 PVKSPRRSSSDQGLSYSSL 556

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RESULT 8

AAU09987
AAU09987 standard; Protein; 512 AA.

AAU09987;

21-MAY-2002 (first entry)

Human IL-1R ACP protein deletion mutant delta C2 #2.

IL-1R ACP; human; interleukin-1 receptor accessory protein; NF-kappaB; IL-1; IL-1RI; mutant; mutein; delta C2; inflammatory response.

Homo sapiens.

US6280955-B1.

28-AUG-2001.

16-DEC-1997; 97US-0991944.

16-DEC-1997; 97US-0991944.

(TUTLA-) TUTLAR INC.

Cao Z;

WPI; 2001-595441/67.

N-PSDB; AAS15608.

Isolated polypeptide designated interleukin receptor accessory

polypeptide is useful for regulating cell function

Disclosure; Page - ; 21pp; English.

This sequence represents the human interleukin-1 receptor accessory protein (IL-1Racp) mutant delta C2 #2 of the invention. This deletion mutant was used to define a phosphorylated domain of the IL-1Racp protein at tyrosine 503. The interleukin receptor accessory protein (IL-1Racp) and its modulators (agonists/antagonists) are useful for regulating cell function. Transient expression of either IL-1RI or IL-1Racp alone does not result in ligand-independent induction of an NF-kappaB-dependent luciferase reporter gene in 293 cells, however coexpression of both proteins resulted in a 20-fold increase in activation of NF-kappaB activity to a level comparable to that induced

by IL-1. These data suggest that aggregation of IL-1RI and IL-1Racp as a result of protein overexpression can elicit a signaling pathway leading to NF-kappaB activation. Modulating signal transduction involving NF-kappaB in a cell may be achieved by modulating the activity of IL-1Racp using binding agents such as agonists and antagonists. Hybridisation probes to the cDNA sequence can be used to identify wild-type and mutant IL-1Racp alleles in clinical and laboratory samples. Mutant alleles are used to generate allele-specific oligonucleotide (ASO) probes for high-throughput clinical diagnoses of diseases or disorders with an inflammatory response. In therapy, therapeutic IL-1Racp nucleic acids are used to modulate cellular expression or intracellular concentration or availability of active IL-1Racp. This invention also comprises a method of screening for an agent that modulates the interaction of an interleukin receptor accessory polypeptide (IL-1Racp) to a binding target.

CC Note: The present sequence is not included in the CC specification but was created from the human IL-1R ACP sequence appearing as AAU09986 and the information given in table 1 of the CC specification.

Sequence 512 AA;

Query Match 68.2%; Score 2502.5; DB 22; Length 512;
Best Local Similarity 92.0%; Pred. No. 1.7e-205;
Matches 469; Conservative 20; Mismatches 14; Indels 7; Gaps 2;

```

QY 1 MTLKMCVSLYFYGILOSDESRCDMDGIDYMQIOVFEDEPARIKCPLEHEFLKENYST 60
DB 1 MTLKMCVSLYFYGILOSDESRCDMDGIDYMQIOVFEDEPARIKCPLEHEFLKENYST 60
QY 61 AHSAGLTLIWMYTRQDRDLEEPINFRLPENRISKEKQVLMFRFTLLANDTGYTCMLRNTT 120
DB 61 AHSAGLTLIWMYTRQDRDLEEPINFRLPENRISKEKQVLMFRFTLLANDTGYTCMLRNTT 120
QY 121 YCSKVAFFLEVVQKDSCFNSPMGLPVHKLIEYGIQRTICPNVDGYFPSSVKPTITWYMG 180
DB 121 YCSKVAFFLEVVQKDSCFNSPMGLPVHKLIEYGIQRTICPNVDGYFPSSVKPTITWYMG 180
QY 181 CYKIONNNVPIPGMNLSPFLIALISNNGNVCTVTPENGRTFHLRLTLTKVVGSPKNA 240
DB 181 CYKIONNNVPIPGMNLSPFLIALISNNGNVCTVTPENGRTFHLRLTLTKVVGSPKNA 240
QY 241 VPEVIHSPNDHVVYVEKERGSELLPCTVYFSFLMDSRNEVWMTIDGKKPDITIDVTINE 300
DB 241 VPEVIHSPNDHVVYVEKERGSELLPCTVYFSFLMDSRNEVWMTIDGKKPDITIDVTINE 300
QY 301 SISHSRTEDTRQOILSIRKVTSEDLKRSYVCHARSAGKGEVAKAKAVKQKVPARYVEL 360
DB 301 SISHSRTEDTRQOILSIRKVTSEDLKRSYVCHARSAGKGEVAKAKAVKQKVPARYVEL 360
QY 361 ACGFGATVLLVLLIVVHYVWLEMLVFLYRAHFGTDETTIDGKEYDIYVSAYARNAEERF 420
DB 361 ACGFGATVLLVLLIVVHYVWLEMLVFLYRAHFGTDETTIDGKEYDIYVSAYARNAEERF 420
QY 421 VLLTLRGVLENERGYKLCIFDRDSLPGQIVTDETLISFLQKSRLLVLSPNVYLQGTAL 480
DB 421 VLLTLRGVLENERGYKLCIFDRDSLPGQIVTDETLISFLQKSRLLVLSPNVYLQGTAL 480
QY 481 LEEFGVGMCONSIATK---LIVVEYRPLE 506
DB 481 LEEFGVGMCONSIATK---LIVVEYRPLE 506

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RESULT 9

AAU09981
AAU09981 standard; Protein; 520 AA.

AAU09981;

21-MAY-2002 (first entry)

Human IL-1R ACP protein deletion mutant delta C4.

KM IL-1R ACP; human; interleukin-1 receptor accessory protein; NF-kappaB;
 KM IL-1; IL-1R1; mutant; mutein; delta C4; inflammatory response.
 XX Homo sapiens.
 OS
 XX
 PN US6280955-B1.
 XX
 PD 28-AUG-2001.
 XX
 PE 16-DEC-1997; 97US-0991944.
 XX
 PR 16-DEC-1997; 97US-0991944.
 XX
 PA (TULAR-) TULARIK INC.
 PI
 DR WPI; 2001-595441/67.
 DR N-PSDB; AAS15608.
 XX
 PT Isolated polypeptide designated interleukin receptor accessory polypeptide is useful for regulating cell function -
 Disclosure; Page - : 21pp; English.

AY This sequence represents the human interleukin-1 receptor accessory protein (IL-1RacP) mutant delta C4 of the invention. This mutant CC was used to define domains of the IL-1RacP protein that have the CC ability to activate NF-kappaB expression. The interleukin receptor CC accessory protein (IL-1RacP) and its modulators (agonists/antagonists) CC are useful for regulating cell function. Transient expression of either CC IL-1R1 or IL-1RacP alone does not result in ligand-independent induction of an NF-kappaB-dependent luciferase reporter gene in 293 cells, however CC coexpression of both proteins resulted in a 20-fold increase in CC activation of NF-kappaB activity to a level comparable to that induced CC by IL-1. These data suggest that aggregation of IL-1R1 and IL-1RacP as CC a result of protein overexpression can elicit a signaling pathway CC leading to NF-kappaB activation. Modulating signal transduction CC involving NF-kappaB in a cell may be achieved by modulating the activity CC of IL-1RacP using binding agents such as agonists and antagonists. CC Hybridisation probes to the cDNA sequence can be used to identify wild- CC type and mutant IL-1RacP alleles in clinical and laboratory CC samples. Mutant alleles are used to generate allele-specific CC oligonucleotide (ASO) probes for high-throughput clinical diagnoses CC of diseases or disorders with an inflammatory response. In CC therapy, therapeutic IL-1RacP nucleic acids are used to modulate CC cellular expression or intracellular concentration or availability of CC active IL-1RacP. This invention also comprises a method of screening for CC an agent that modulates the interaction of an interleukin receptor CC accessory polypeptide (IL-1RacP) to a binding target.
 Note: The present sequence is not included in the CC specification but was created from the human IL-1R ACP sequence CC appearing as A4009366 and the information given in table 1 of the CC specification.
 CC
 XX
 XX
 SQ Sequence 520 AA;

Query Match 68.2%; Score 2502.5; DB 22; Length 520;
 Best Local Similarity 92.0%; Pred. No. 1.8e-205;
 Matches 469; Conservative 20; Mismatches 14; Indels 7; Gaps 2;

QY 1 MTLAMCVSLKFFYGLSDASERCDMDLDTMROIOVEDPSPARKICLFEHFLKENST 60
 DB 1 MTLAMCVSLKFFYGLSDASERCDMDLDTMROIOVEDPSPARKICLFEHFLKENST 60
 QY 61 AHSAGLTLLIWMYTRQDRDLDEEPINFRLEPNRISKEKDVLMFRPTLLNDTGNVTCMLRNTT 120
 DB 61 AHSAGLTLLIWMYTRQDRDLDEEPINFRLEPNRISKEKDVLMFRPTLLNDTGNVTCMLRNTT 120
 QY 121 YCSVAAPLEVVQDSCNSPMKLPVHGLYIEYGIQRTICNVVDGYFPSSVYKPTITWYMG 180
 DB 121 YCSVAAPLEVVQDSCNSPMKLPVHGLYIEYGIQRTICNVVDGYFPSSVYKPTITWYMG 180

QY 181 CYKIQNFNNVPEBGMNISFLIALISNNNGNTCVVYTPENGRTFHLTRTLTKVVGSPKNA 240
 DB 181 CYKIQNFNNVPEBGMNISFLIALISNNNGNTCVVYTPENGRTFHLTRTLTKVVGSPKNA 240
 QY 241 VPPVISHPNDDHVVYKEKGESELLPCTVYFSPFLMDSNREVMWTIDGKCPDITIDVTINE 300
 DB 241 VPPVISHPNDDHVVYKEKGESELLPCTVYFSPFLMDSNREVMWTIDGKCPDITIDVTINE 300
 QY 301 SISHRTEDETFRTOILSISKVYTSDDLKRSYVCARSAKSGVAAAKKQVAPARYVEL 360
 DB 301 SISHRTEDETFRTOILSISKVYTSDDLKRSYVCARSAKSGVAAAKKQVAPARYVEL 360
 QY 361 ACGFATVLLVLIIVVHYVWLEMLFYRAHFGTDETIIDGKEYDLYVYARAAEEEF 420
 DB 361 ACGFATVLLVLIIVVHYVWLEMLFYRAHFGTDETIIDGKEYDLYVYARAAEEEF 420
 QY 421 VLLTRGVLENEFGYKLCIFDRDRLPGGNTVEAVDFIQSRNMIVLSPDYTEKSI 480
 DB 421 VLLTRGVLENEFGYKLCIFDRDRLPGGNTVEAVDFIQSRNMIVLSPDYTEKSI 480
 QY 481 LEFKLQVMCONSLTK---LIYVETRPLE 506
 DB 481 LEFKLQVMCONSLTK---LIYVETRPLE 506
 DB 481 LEFKLQVMCONSLTK---LIYVETRPLE 506

RESULT 10
 AAM01913
 ID AAM01913 standard; Protein; 570 AA.
 XX
 AC AAM01913;
 XX
 DT 14-OCT-1996 (first entry)
 XX
 DE Mouse interleukin-1 receptor accessory protein.
 XX
 KM Interleukin-1 receptor accessory protein; IL-1 antagonist;
 KM inflammation; therapy; antiinflammatory; antibody;
 KM rheumatoid arthritis; inflammatory bowel disease; septic shock;
 KM transplant rejection; psoriasis; asthma; type 1 diabetes;
 KM cancer; leukaemia.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT Protein /label= Sig_peptide
 FT /label= 21..570
 FT Domain /label= Mat_protein
 FT /label= 21..359
 FT Domain /label= Extracellular_domain
 FT Domain /label= 360..383
 FT Domain /label= Transmembrane_domain
 FT Domain /label= 384..570
 FT /label= Cytoplasmic_tail
 XX
 PN NO9623067-A1.
 XX
 PD 01-AUG-1996.
 XX
 PF 17-JAN-1996; 96MO-EP00181.
 XX
 PR 23-JAN-1995; 95US-0376268.
 XX
 PA (HOPF) HOPFMANN LA ROCHE & CO AG F.
 XX
 PI Chizzonite RA, Ju GW;
 DR WPI; 1996-362681/36.
 DR N-PSDB; AAT32028.
 XX
 PT Isolated interleukin-1 receptor accessory protein - used to develop
 PT prods. to treat or prevent inflammatory or immunological activities
 PT of interleukin-1

XX Example 7; Page 78-80; 115pp; English.

PS Mouse interleukin-1 receptor accessory protein (IL-1R ACP) (AA001913)
 CC is a protein that inhibits the ability of IL-1 to bind to, or
 CC otherwise activate, the IL-1R, esp. the Type 1 IL-1R. Its amino
 CC acid sequence was deduced from a cDNA clone (AA032028) derived
 CC from 3R3-11 cells. A human homologue (AA001911) of the IL-1R ACP
 CC has been isolated that is useful in modulating the inflammatory
 CC and immunological activities of human IL-1.

XX Sequence 570 AA;

Query Match 63.4%; Score 2327.5; DB 17; Length 570;
 Best Local Similarity 75.9%; Pred. No. 2e-190;
 Matches 429; Conservative 66; Mismatches 55; Indels 15; Gaps 5;

1 MTLWCVSLVYFYGIQSDASERCDWGLDTMRQIQVFEDEPARIKCPLEHFLKFNST 60
 1 MGLMTYMSLSFYGIQSHASERCDWGLDTMRQIQVFEDEPARIKCPLEHFLKFNST 60
 61 AHSAGTLIWTWTRQDRDLSEEPINFRLEPNRISKEDVLMFRPTLNDGNTQMLRNTT 120
 61 AHSAGTLIWTWTRQDRDLSEEPINFRLEPNRISKEDVLMFRPTLNDGNTQMLRNTT 120
 121 YCSKVAFLVAVQKSCFNSPMKLPHKLYIEGRIQITCPNVGYPSSVAKPTITWYG 180
 121 YCSKVAFLVAVQKSCFNSPMKLPHKLYIEGRIQITCPNVGYPSSVAKPTITWYG 180
 181 CYKIONFNNVPIEGNLSFLIALISNNGNYTCVTPYENGRTFHLTRTLTKVVGSPKNA 240
 181 CTEIVDFHNVLPBGNLSFPIPLVSNNGNYTCVTPYENGRTFHLTRTLTKVVGSPKNA 240
 241 VPPVHSPNDVHYEKEGEBELIPCTVYFSLMDSRNEVWTTIDGKDDITDVTINE 300
 241 LPQIYSPNDRVYKEGEBELIPCKVYFSLMDSRNEVWTTIDGKDDITDVTINE 300
 301 SISHRTEDERTQILSIKKTSEDLSKSYVCHASAKGEVAKAAKVKQKVPARYTEL 360
 301 SVSYSTEDERTQILSIKKTSEDLSKSYVCHASAKGEVAKAAKVKQKVPARYTEL 360
 361 ACQFGATVLLVYLIVVHYVWLEWLFYRAHFGTDETLIDGKDYIYVSARNAEEEF 420
 361 ACQFGATVLLVYLIVVHYVWLEWLFYRAHFGTDETLIDGKDYIYVSARNAEEEF 420
 421 VLLTRGVLENERGYLCTIPDRDSLPGGIVTDETLSFIQSRRLVVLSPNYLQCTQAL 480
 421 VLLTRGVLENERGYLCTIPDRDSLPGGIVTDETLSFIQSRRLVVLSPNYLQCTQAL 480
 481 LEFKGVGMGNSIATK---LIVVEYRPLEHHPGLQKES---VSFYSWKGSKSHG 533
 481 LEFKAGL---ENNASGNINVLIVQKAVKDK--VKEILKRAKTVLTVIKMGESKSYPO 535
 534 SKFWKRLALPLRLSLASSGNNS 558
 536 GRFWKQLQVAMPVK---SPRMSN 557

RESULT 11
 ID AA00967 standard; Protein; 570 AA.
 AC AA00967;
 XX 21-MAY-2002 (first entry)
 DT Mouse interleukin-1 Receptor accessory protein (IL-1R ACP) protein.
 XX Mouse interleukin-1 Receptor accessory protein (IL-1R ACP) protein.
 DE IL-1R ACP; mouse; interleukin-1 receptor accessory protein; NF-kappaB;
 KM IL-1; IL-1R; inflammatory response.
 OS Mus sp.
 XX

PN US6280955-B1.
 XX 28-AUG-2001.
 PD 16-DEC-1997; 97US-0991944.
 XX 16-DEC-1997; 97US-0991944.
 PF 16-DEC-1997; 97US-0991944.
 XX (TULA-) TULARIK INC.
 PA Cao Z;
 XX WPI; 2001-595441/67.
 DR N-PSDB; AAS15609.
 XX Isolated polypeptide designated interleukin receptor accessory
 PT polypeptide is useful for regulating cell function
 PS Disclosure; Fig 1; 21pp; English.

This sequence represents the mouse interleukin-1 receptor accessory protein (IL-1R ACP), the cDNA sequence for this protein was used to generate a hybridisation probe that was used to isolate the human IL-1R ACP cDNA sequence of the invention. The interleukin-1 receptor accessory protein (IL-1R ACP) and its modulators (agonists/antagonists) are useful for regulating cell function. Transient expression of either IL-1R1 or IL-1R ACP alone does not result in ligand-independent induction of an NF-kappaB-dependent luciferase reporter gene in 293 cells, however coexpression of both proteins resulted in a 20-fold increase in activation of NF-kappaB activity to a level comparable to that induced by IL-1. These data suggest that aggregation of IL-1R1 and IL-1R ACP as a result of protein overexpression can elicit a signaling pathway leading to NF-kappaB activation. Modulating signal transduction involving NF-kappaB in a cell may be achieved by modulating the activity of IL-1R ACP using binding agents such as agonists and antagonists. Hybridisation probes to the cDNA sequence can be used to identify wild-type and mutant IL-1R ACP alleles in clinical and laboratory samples. Mutant alleles are used to generate allele-specific oligonucleotide (ASO) probes for high-throughput clinical diagnoses of diseases or disorders with an inflammatory response. In therapy, therapeutic IL-1R ACP nucleic acids are used to modulate cellular expression or intracellular concentration or availability of active IL-1R ACP. This invention also comprises a method of screening for an agent that modulates the interaction of an interleukin receptor accessory polypeptide (IL-1R ACP) to a binding target.

Query Match 63.4%; Score 2327.5; DB 22; Length 570;
 Best Local Similarity 75.9%; Pred. No. 2e-190;
 Matches 429; Conservative 66; Mismatches 55; Indels 15; Gaps 5;

1 MTLWCVSLVYFYGIQSDASERCDWGLDTMRQIQVFEDEPARIKCPLEHFLKFNST 60
 1 MGLMTYMSLSFYGIQSHASERCDWGLDTMRQIQVFEDEPARIKCPLEHFLKFNST 60
 61 AHSAGTLIWTWTRQDRDLSEEPINFRLEPNRISKEDVLMFRPTLNDGNTQMLRNTT 120
 61 AHSAGTLIWTWTRQDRDLSEEPINFRLEPNRISKEDVLMFRPTLNDGNTQMLRNTT 120
 121 YCSKVAFLVAVQKSCFNSPMKLPHKLYIEGRIQITCPNVGYPSSVAKPTITWYG 180
 121 YCSKVAFLVAVQKSCFNSPMKLPHKLYIEGRIQITCPNVGYPSSVAKPTITWYG 180
 181 CYKIONFNNVPIEGNLSFLIALISNNGNYTCVTPYENGRTFHLTRTLTKVVGSPKNA 240
 181 CTEIVDFHNVLPBGNLSFPIPLVSNNGNYTCVTPYENGRTFHLTRTLTKVVGSPKNA 240
 241 VPPVHSPNDVHYEKEGEBELIPCTVYFSLMDSRNEVWTTIDGKDDITDVTINE 300
 241 LPQIYSPNDRVYKEGEBELIPCKVYFSLMDSRNEVWTTIDGKDDITDVTINE 300
 301 SISHRTEDERTQILSIKKTSEDLSKSYVCHASAKGEVAKAAKVKQKVPARYTEL 360

CC an agent that modulates the interaction of an interleukin receptor
 CC accessory polypeptide (IL-1R α) to a binding target.
 CC Note: The present sequence is not included in the
 CC specification but was created from the human IL-1R ACP sequence
 CC appearing as A409966 and the information given in table 1 of the
 CC specification.

XX Sequence 501 AA:

Query Match 60.3%; Score 2212; DB 22; Length 501;
 Best Local Similarity 83.3%; Pred. No. 1.3e-180;
 Matches 419; Conservative 35; Mismatches 37; Indels 12; Gaps 4;

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Oy 70 WWTRODRLPEEPINRLPENRISKEKDVLMFRPTLLNDGNTGNTCMRLRTYTCSSVAPRL 129
Db 1 WWTRODRLPEEPINRLPENRISKEKDVLMFRPTLLNDGNTGNTCMRLRTYTCSSVAPRL 60
Oy 130 EVVQKDCSCNSPMKLPVHKLYIEYGIQRTCPNVDGFPSSVAPRTTWGCVKIQNFNN 189
Db 61 EVVQKDCSCNSPMKLPVHKLYIEYGIQRTCPNVDGFPSSVAPRTTWGCVKIQNFNN 120
Oy 190 VIREGNLISFLIALISNNGNTCVTPYPPNGRTFHLTRITLVKVGSPKNAVPPVTHSPN 249
Db 121 VIREGNLISFLIALISNNGNTCVTPYPPNGRTFHLTRITLVKVGSPKNAVPPVTHSPN 180
Oy 250 DHVYVKEKEGEBELLIPCTYVFFSLMDSRNEVMTIDGKRPDDITDVTINESIHSRTD 309
Db 181 DHVYVKEKEGEBELLIPCTYVFFSLMDSRNEVMTIDGKRPDDITDVTINESIHSRTD 240
Oy 310 ERTTOILSKKTSYEDLKSRYCHASAGVAKAKVOKVAPRYTELACGFATYL 369
Db 241 ERTTOILSKKTSYEDLKSRYCHASAGVAKAKVOKVAPRYTELACGFATYL 300
Oy 370 LVVILIVVHVYLVEMVLFYRAHFGTDETLIDGKEYDIYVSARNAEPEFVLLTLRGLV 429
Db 301 LVVILIVVHVYLVEMVLFYRAHFGTDETLIDGKEYDIYVSARNAEPEFVLLTLRGLV 360
Oy 430 ENEERGKLCIFPRDSIPGANTVAVDPFIOQRSMITVLSPEYVTEKSIISMLEFELGVNC 489
Db 361 ENEERGKLCIFPRDSIPGANTVAVDPFIOQRSMITVLSPEYVTEKSIISMLEFELGVNC 418
Oy 490 QNSIATK---LIVVEKRPLEHHPGILDKES---VSFVSWGSEKSKSGKFWALRL 542
Db 419 -EMASRGMINIVLVOKAVKTK--VKELAKKATVLYVIKMGESKXIPQGRFVKQLQV 475
Oy 543 ALPLRLSLASGWNSSCCSQSDI 565
Db 476 AMPVKKSPRRSSDEQGLSYSSL 498

TLT 15
J1912
AAW01912 standard; Protein; 359 AA.
AAW01912;
XX
XX
XX 14-OCT-1996 (first entry)
Db
XX Soluble interleukin-1 receptor accessory protein.
XX
XX Interleukin-1 receptor accessory protein; IL-1 antagonist;
XX inflammation; therapy; antiinflammatory; antibody;
XX rheumatoid arthritis; inflammatory bowel disease; septic shock;
XX transplant rejection; psoriasis; asthma; type 1 diabetes;
XX cancer; leukaemia.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Peptide 1..20
XX FT /label= Sig_peptide
XX FT 21..359
XX FT Domain /label= Extracellular_domain

```

```

XX
XX M09623067-A1.
XX
XX 01-AUG-1996.
XX
XX 17-JAN-1996; 96WO-EP00181.
XX
XX 23-JAN-1995; 95US-0376268.
XX
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX Chizzone RA, Ju GW;
XX WPI; 1996-362691/36.
XX N-PSDB; AAT32027.
XX
XX Isolated interleukin-1 receptor accessory protein - used to develop
XX of interleukin-1
XX
XX Claim 8; Page 82-83; 115pp; English.
XX
XX A soluble form (AAW01912) of human interleukin-1 receptor
XX accessory protein (IL-1R ACP) (AAW01911) lacks the transmembrane
XX domain and cytoplasmic tail of the native protein (see also
XX AAW01911). It can be obtd. using a cDNA clone (AAT32027) produced
XX by PCR amplification (see also AAT32029-30) of human IL-1R ACP
XX cDNA, and expression using e.g. a baculovirus system in Sf9
XX insect cells. The soluble protein is partic. useful in
XX preventing the inflammatory or immunological activities of IL-1,
XX esp. for the treatment of rheumatoid arthritis, inflammatory bowel
XX disease, septic shock, transplant rejection, psoriasis, asthma,
XX type 1 diabetes or acute and chronic myelogenous leukaemia, and
XX can also be used to screen potential IL-1 antagonists.
XX
XX Sequence 359 AA:
SQ

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Query Match 52.7%; Score 1934; DB 17; Length 359;
 Best Local Similarity 99.7%; Pred. No. 5.2e-157;
 Matches 358; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Oy 1 MTLKCVSLVFGYGIQSDASERCDMDGIDTMRQIOVEDEPARIKCPLFEHFLKFNST 60
Db 1 MTLKCVSLVFGYGIQSDASERCDMDGIDTMRQIOVEDEPARIKCPLFEHFLKFNST 60
Oy 61 AHSAGTLITWTRODRLPEEPINRLPENRISKEKDVLMFRPTLLNDGNTGNTCMRLRT 120
Db 61 AHSAGTLITWTRODRLPEEPINRLPENRISKEKDVLMFRPTLLNDGNTGNTCMRLRT 120
Oy 121 YCSKAPFLVAVQKDCSCNSPMKLPVHKLYIEYGIQRTCPNVDGFPSSVAPRTTWG 180
Db 121 YCSKAPFLVAVQKDCSCNSPMKLPVHKLYIEYGIQRTCPNVDGFPSSVAPRTTWG 180
Oy 181 CYKIQNFNNVIREGNLISFLIALISNNGNTCVTPYPPNGRTFHLTRITLVKVGSPKNA 240
Db 181 CYKIQNFNNVIREGNLISFLIALISNNGNTCVTPYPPNGRTFHLTRITLVKVGSPKNA 240
Oy 241 VPPVTHSPNDHVYVKEKEGEBELLIPCTYVFFSLMDSRNEVMTIDGKRPDDITDVTINE 300
Db 241 VPPVTHSPNDHVYVKEKEGEBELLIPCTYVFFSLMDSRNEVMTIDGKRPDDITDVTINE 300
Oy 301 SISHRTDETRTOILSKKTSYEDLKSRYCHASAGVAKAKVOKVAPRYTELACGFATYL 359
Db 301 SISHRTDETRTOILSKKTSYEDLKSRYCHASAGVAKAKVOKVAPRYTELACGFATYL 359

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Search completed: April 23, 2003, 08:51:43
 Job time : 44 secs

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 23, 2003, 08:51:01 ; Search time 30 Seconds

(Without alignments)
673.785 Million cell updates/sec

Title: US-10-061-727-2

Perfect score: 3669

Sequence: 1 MTLWCVSYLFFGILQSDA.....SALALHFTDLSNNDFYIL 687

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/aa/5A COMB.pep.*
2: /cgn2_6/prodata/1/aa/5B COMB.pep.*
3: /cgn2_6/prodata/1/aa/6A COMB.pep.*
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5: /cgn2_6/prodata/1/aa/PCTUS COMB.pep.*
6: /cgn2_6/prodata/1/aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2586	70.5	570	4	US-08-991-944-2
2	2586	70.5	570	4	US-09-173-151A-36
3	2327.5	63.4	570	4	US-08-991-944-4
4	2327.5	63.4	570	4	US-09-173-151A-21
5	825	22.5	686	4	US-09-173-151A-4
6	800	21.8	579	4	US-09-173-151A-2
7	762.5	20.8	668	4	US-09-173-151A-35
8	528	14.4	541	1	US-08-604-333-2
9	528	14.4	541	3	US-09-110-618-2
10	528	14.4	541	4	US-09-173-151A-28
11	520	14.2	521	3	US-08-996-338-20
12	496	13.5	555	1	US-07-821-716-4
13	484.5	13.2	576	1	US-08-381-603-4
14	484.5	13.2	576	2	US-08-924-376-4
15	484.5	13.2	576	4	US-08-685-212-4
16	484.5	13.2	576	4	US-09-173-151A-30
17	484.5	13.2	576	4	US-08-466-932A-4
18	484.5	13.2	576	5	PCT-US94-02414-4
19	484.5	13.2	576	5	PCT-US96-08899-4
20	484.5	13.2	576	3	US-08-604-333-4
21	479	13.1	537	1	US-09-110-618-4
22	479	13.1	537	3	US-09-173-151A-29
23	479	13.1	537	4	US-09-173-151A-2
24	479	13.1	537	4	US-08-996-338-21
25	478	13.0	567	4	US-09-560-639-7
26	478	13.0	567	4	US-09-560-639-7
27	478	13.0	567	4	US-09-560-639-7

28	478	13.0	567	4	US-09-173-151A-24	Sequence 24, Appl
29	478	13.0	567	4	US-09-032-337-39	Sequence 39, Appl
30	471.5	12.9	599	4	US-09-173-151A-10	Sequence 10, Appl
31	463.5	12.6	556	4	US-09-560-639-8	Sequence 8, Appl
32	457	12.5	561	4	US-09-227-717-4	Sequence 4, Appl
33	457	12.5	561	4	US-09-173-151A-23	Sequence 23, Appl
34	446	12.2	614	4	US-09-173-151A-16	Sequence 16, Appl
35	445	12.1	610	4	US-09-173-151A-14	Sequence 14, Appl
36	444.5	12.1	562	4	US-09-227-717-2	Sequence 2, Appl
37	444.5	12.1	562	4	US-09-173-151A-22	Sequence 22, Appl
38	436	11.9	467	4	US-09-173-151A-8	Sequence 8, Appl
39	424.5	11.6	569	1	US-07-821-716-2	Sequence 2, Appl
40	424.5	11.6	569	2	US-08-381-603-2	Sequence 2, Appl
41	424.5	11.6	569	4	US-08-924-376-2	Sequence 2, Appl
42	424.5	11.6	569	4	US-08-685-212-2	Sequence 2, Appl
43	424.5	11.6	569	4	US-09-173-151A-31	Sequence 31, Appl
44	424.5	11.6	569	4	US-08-466-932A-2	Sequence 2, Appl
45	424.5	11.6	569	5	PCT-US94-02414-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-991-944-2

Sequence 2, Application US/08991944
Patent No. 6280955

GENERAL INFORMATION:

APPLICANT: Cao, Zhaodan

TITLE OF INVENTION: Interleukin-1 Receptor Accessory Proteins,

TITLE OF INVENTION: Nucleic Acids and Methods

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 75 DENISE DRIVE

CITY: HILLSBOROUGH

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94010

COMPUTER RELEASABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/991,944

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: T97-014

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 343-4341

TELEFAX: (650) 343-4342

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 570 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-991-944-2

Query Match

Best Local Similarity: 85.3%; Pred. No. 2.8e-244;

Matches 488; Conservative: 35; Mismatches 37; Indels 12; Gaps 4;

QY 1 MTLWCVSYLFFGILQSDA.....SALALHFTDLSNNDFYIL 687
DB 1 MTLWCVSYLFFGILQSDA.....SALALHFTDLSNNDFYIL 687
QY 61 AHSAGTLTIWYTRQDRLDEPINFLLPENRISKEKQVLFRRPTLLANDTGYTCLMNTT 120

Thu May 1 09:36:18 2003

us-10-061-727-2.ra1

Page 2

Db 61 AHSAGLTLIMWTRQDRDLDEEPINFLPENRISKEDVLMFRPTLLNDGNTYCMLENTT 120
Qy 121 YCSKVAFPLEVQKSCFNSPKMLPVHKLITYEGIORICPNVDGYPPSSVKTITWYG 180
Db 121 YCSKVAFPLEVQKSCFNSPKMLPVHKLITYEGIORICPNVDGYPPSSVKTITWYG 180
Qy 181 CYKIQFNFNVIPEGNMLSLFIALISNNGNTCVVTPENGRTFHLTRLTVKVGSPKXA 240
Db 181 CYKIQFNFNVIPEGNMLSLFIALISNNGNTCVVTPENGRTFHLTRLTVKVGSPKXA 240
Qy 241 VPPVHSPNDHVVYEKEPEBEILLICTVYFSLMDSRNEVMTIDGKEDDITIDVTINE 300
Db 241 VPPVHSPNDHVVYEKEPEBEILLICTVYFSLMDSRNEVMTIDGKEDDITIDVTINE 300
Qy 301 SISHSTEDETRQIISIKKVTSEDLKRSYVCHARSAKGVAAKAVKOKVAPRYVEL 360
Db 301 SISHSTEDETRQIISIKKVTSEDLKRSYVCHARSAKGVAAKAVKOKVAPRYVEL 360
Qy 361 ACGFGATVLLVLLIVVHYVWLEWVLFYRAHFGTDETLIDGKEYDIYVSARNAEEEF 420
Db 361 ACGFGATVLLVLLIVVHYVWLEWVLFYRAHFGTDETLIDGKEYDIYVSARNAEEEF 420
Qy 421 VLLTTRGVLNENRGYKLCIFDRDSLPGNTVEAVDFIORSRRIIVLSPDYVTEKISIM 480
Db 421 VLLTTRGVLNENRGYKLCIFDRDSLPGNTVEAVDFIORSRRIIVLSPDYVTEKISIM 480
Qy 481 LEPKLGVMONSIATK---LIVVEYRPLEHPHPIQLKES--VSFVSMKGEKSKYHG 533
Db 481 LEPKLGVMONSIATK---LIVVEYRPLEHPHPIQLKES--VSFVSMKGEKSKYHG 533
Qy 534 SKFWKALRLALPLRLSASGNNESCSQSDI 565
Db 536 GRFWKQLQVAMPVKSPRRSSDDEGLSYSSL 567

RESULT 2

US-09-173-151A-36
Sequence 36, Application US/09173151A
Patent No. 6326472
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
APPLICANT: Debers, Johannes Eduard Maria
APPLICANT: Antonius
APPLICANT: Sana, Theodore R.
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: DMAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,151A
FILING DATE: 14-OCT-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Chung, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-9196
FAX: (650) 496-1200
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 570 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-173-151A-36

Query Match 70.5% Score 2586; DB 4; Length 570;

Best Local Similarity 85.3% Pred. No. 2.8e-244; Mismatches 37; Indels 12; Gaps 4;

Matches 488; Conservative 35; Mismatches 37; Indels 12; Gaps 4;

Qy 1 MTLMLCVSLVYFYGLIQSDASERCDMDGLTWROIQVEFEDEPARIKCPLFEHLKFNYST 60
Db 1 MTLMLCVSLVYFYGLIQSDASERCDMDGLTWROIQVEFEDEPARIKCPLFEHLKFNYST 60
Qy 61 AHSAGLTLIMWTRQDRDLDEEPINFLPENRISKEDVLMFRPTLLNDGNTYCMLENTT 120
Db 61 AHSAGLTLIMWTRQDRDLDEEPINFLPENRISKEDVLMFRPTLLNDGNTYCMLENTT 120
Qy 121 YCSKVAFPLEVQKSCFNSPKMLPVHKLITYEGIORICPNVDGYPPSSVKTITWYG 180
Db 121 YCSKVAFPLEVQKSCFNSPKMLPVHKLITYEGIORICPNVDGYPPSSVKTITWYG 180
Qy 181 CYKIQFNFNVIPEGNMLSLFIALISNNGNTCVVTPENGRTFHLTRLTVKVGSPKXA 240
Db 181 CYKIQFNFNVIPEGNMLSLFIALISNNGNTCVVTPENGRTFHLTRLTVKVGSPKXA 240
Qy 241 VPPVHSPNDHVVYEKEPEBEILLICTVYFSLMDSRNEVMTIDGKEDDITIDVTINE 300
Db 241 VPPVHSPNDHVVYEKEPEBEILLICTVYFSLMDSRNEVMTIDGKEDDITIDVTINE 300
Qy 301 SISHSTEDETRQIISIKKVTSEDLKRSYVCHARSAKGVAAKAVKOKVAPRYVEL 360
Db 301 SISHSTEDETRQIISIKKVTSEDLKRSYVCHARSAKGVAAKAVKOKVAPRYVEL 360
Qy 361 ACGFGATVLLVLLIVVHYVWLEWVLFYRAHFGTDETLIDGKEYDIYVSARNAEEEF 420
Db 361 ACGFGATVLLVLLIVVHYVWLEWVLFYRAHFGTDETLIDGKEYDIYVSARNAEEEF 420
Qy 421 VLLTTRGVLNENRGYKLCIFDRDSLPGNTVEAVDFIORSRRIIVLSPDYVTEKISIM 480
Db 421 VLLTTRGVLNENRGYKLCIFDRDSLPGNTVEAVDFIORSRRIIVLSPDYVTEKISIM 480
Qy 481 LEPKLGVMONSIATK---LIVVEYRPLEHPHPIQLKES--VSFVSMKGEKSKYHG 533
Db 481 LEPKLGVMONSIATK---LIVVEYRPLEHPHPIQLKES--VSFVSMKGEKSKYHG 533
Qy 534 SKFWKALRLALPLRLSASGNNESCSQSDI 565
Db 536 GRFWKQLQVAMPVKSPRRSSDDEGLSYSSL 567

RESULT 3

US-08-991-944-4
Sequence 4, Application US/08991944

Patent No. 6280955
GENERAL INFORMATION:
APPLICANT: Cao, Zhaoan
TITLE OF INVENTION: Interleukin-1 Receptor Accessory Proteins,
TITLE OF INVENTION: Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,944
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-014
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 570 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
US-08-991-944-4

Query Match 63.4%; Score 2327.5; DB 4; Length 570;
Best Local Similarity 75.9%; Pred. No. 5.7e-219;
Matches 429; Conservative 66; Mismatches 55; Indels 15; Gaps 5;

QY 1 MTLIMCVSLVYFGILSDASERCDDMLDTMROIOVEDEBPARKCPLFHHFLKFNST 60
1 MGLIMYMSISFYGLDSHASERCDDMLDTMROIOVEDEBPARKCPLFHHFLKFNST 60
DB 1 MGLIMYMSISFYGLDSHASERCDDMLDTMROIOVEDEBPARKCPLFHHFLKFNST 60
61 AHSAGLTILMTWTRODRDLPEPINFRLPENRISKEKDVLMFRPTLNDTGYTCMLRNTT 120
DB 61 AHSAGLTILMTWTRODRDLPEPINFRLPENRISKEKDVLMFRPTLNDTGYTCMLRNTT 120
QY 121 YCSFVAPLEEVOKSCFNSPMKLPVHRLYIEGQRTCPNVGSPSSVKPTITWYMG 180
DB 121 YCSFVAPLEEVOKSCFNSPMKLPVHRLYIEGQRTCPNVGSPSSVKPTITWYMG 180
QY 181 CYKIONFNINVLPEGMNLSFLALISNNNGNYCVVTPYENGRTFHLTRITLVKVGSPKNA 240
DB 181 CTEIVDFNVLPEGMNLSFLALISNNNGNYCVVTPYENGRTFHLTRITLVKVGSPKNA 240
QY 241 VPPVTHSPNDHVVYKEKEBELLPCTVYFSLMDSRNEVMTDGGKPDITDVTINE 300
DB 241 LPQIYSFNDHVVYKEKEBELLPCTVYFSLMDSRNEVMTDGGKPDITDVTINE 300
QY 301 SISHSRTEDERTOLISIKYTSSEDIKRSVYCHASAGFVAKAKVOKXIPARTYVEL 360
DB 301 SISHSRTEDERTOLISIKYTSSEDIKRSVYCHASAGFVAKAKVOKXIPARTYVEL 360
QY 361 ACGFATVLLVILIVVHVLMVLEMLFYRAHFGTDETLIDGKEVDIVSYARNAEEBEF 420
DB 361 ACGFATVLLVILIVVHVLMVLEMLFYRAHFGTDETLIDGKEVDIVSYARNAEEBEF 420
QY 421 VLLTLRGVLENEFGYKLCIFDRDSLPGGNTVEAVFDIQRSRMI VLSLSPDYTERKISM 480
DB 421 VLLTLRGVLENEFGYKLCIFDRDSLPGGNTVEAVFDIQRSRMI VLSLSPDYTERKISM 480

QY 481 LEFKGVMCNSIATK----LIVVEYRLEPHRGLQLKES---VSFVSKGKGRKSG 533
DB 481 LEFKAGL---ENMASRNNIVILVQYKAVDMK--VELBRKTVLTVIKGKGRKVPQ 535
QY 534 SKYKALRLALPLRSLSASGKNES 558
DB 536 GRFWKQLQVAMPVK--SPRWSSN 557

RESULT 4
US-09-173-151A-21
Sequence 21, Application US/09173151A
Patent No. 6326472
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
APPLICANT: Debets, Johannes Eduard Maria
APPLICANT: Antonius
APPLICANT: Sana, Theodore R.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,151A
FILING DATE: 14-OCT-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 570 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULAR TYPE: peptide
US-09-173-151A-21

Query Match 63.4%; Score 2327.5; DB 4; Length 570;

Thu May 1 09:36:18 2003

us-10-061-727-2.ra1

Page 4

Best Local Similarity 75.9%; Pred. No. 5.7e-219;
Matches 429; Conservative 66; Mismatches 55; Indels 15; Gaps 5;

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QY      1 MTLACVSLKEFYGLSDASERCDDMDLPMROIQVFEDEPAIKCPLEFHLKFNVT    60
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      1 MGLMTLYMSLFYTGILGDSHASERCDDMDLPMROIQVFEDEPAIKCPLEFHLKFNIST    60
QY      61 AHSAGLTLIWWTTRDRLDRLEPINFRLPENRISSEKVDLMFRPTLLNDTNGYTCLMRNTT    120
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      61 AHSGLTLIWTTRDRLDRLEPINFRLPENRISSEKVDLMFRPTLLNDTNGYTCLMRNTT    120
QY      121 YCSKAPELLEVQKDCSCNSPMKLPHKLYIEYGIQRITCENVVGYPSSVKPRTTYMG    180
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      121 YCSKAPELLEVQKDCSCNSAMRFVHMVYIEHGIHKITCNVDGYFPSSVKPSVTWKYG    180
QY      181 CYKIONENNVIPEGNNLSFLALTSNNGNATCVUTYPENGRTFHLTRLTLTKVVGSPDNA    240
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      181 CTEIVDFPNVLPEGNNLSFPLPLVSNNGNATCVUTYPENGRLFHLTRLTVTKVVGSPDXA    240
QY      241 VPPVLISHENDHVVEKEEGEBELLPCITYFSFLMDSRNREVMWTIDGKKDDITTDVTINE    300
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      241 LPQIYSNDNRVVYEKEGEELVIPCXYPFSEFINDSHNHEWMITIDGKKDDIVYTDITINE    300
QY      301 SISHRTEDEFRTQIISIKVTSBEDLKESYYCHASAKGEVAKAKAVKQVPARYTEL    360
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      301 SVSYSTEDERTQTQIISKVTPEDLRBNRYCHANRTKGAEQAOKVAPRYTEL    360
QY      361 ACGRGATVLLVILLVNYHWYWLMEVLYYRAHFGTETILLDGKEYDIVYSARNAEBEF    420
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      361 ACGRGATVFLVLLLVNYHWYWLMEVLYYRAHFGTETILLDGKEYDIVYSARNVBEBF    420
QY      421 VLLTLRGVLNEBFGKLCIFPDSDLPGGNTVEAVDPFORSRRMLVLSPPYTEKSISM    480
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      421 VLLTLRGVLNEBFGKLCIFPDSDIPGGIVDETISFIQKSRRLVLVSPPYVLOCTOL    480
QY      481 LEFKLVNCONSIAK---LIVEYRPLEHPHPGIIQLKES--VSFVSWKGSKRSG    533
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      481 LELKAGL---ENMASRGINIVILVOYKAVKOMK--VKELKQAKTVLTVIKWGERSKYQP    535
QY      534 SKFWKALFLALPLRLSLSASSGNES    538
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      536 GRFMKOLQVAMPVKX---SPRWSSN    557

RESULT 5
US-09-173-151A-4
Sequence 4, Application US/09173151A
Patent No. 6326472
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
APPLICANT: Debets, Johannes Eduard Maria
APPLICANT: Antonius
APPLICANT: Sana, Theodore R.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kasteleijn, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173.151A
FILING DATE: 14-OCT-1998
CLASSIFICATION: 435

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PRIOR APPLICATION DATA: US 60/065,776
FILING DATE: 17-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX067X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-9196
TELEFAX: (650) 496-1200
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 686 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-173-151A-4

Query Match 22.5%; Score 825; DB 4; Length 686;
Best Local Similarity 31.9%; Pred. No. 1e-71;
Matches 228; Conservative 106; Mismatches 244; Indels 136; Gaps 27;

1 MTLMWC-VSLIYFGILSDASERCDMDGLTMRQIQVFDEDPARIKCPLEHPLKFNYIS 59
D :|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 7 LALVNCVSSTNLKKWNSGRNVDGIDMSVP-LKTYMALAGSPARKVALTYSTRINYIS 65

60 TAAHSAGLTIIMWTRODRDLPEEIPNFRLPENRSIKEDVLWFRTLLANDTGNTCMLRN 119
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 66 TAQSIGLALMY--KNKDLEELPIIF--SVRRMSEBDSIWPHSADSGFTTCVLANS 121

120 TYCSVAEPFLVEVQRDS--CRNSPMKLFEHKLIYEYG---IQRTGVNDGYPPSSVKP 173
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 122 TYCMKVSMSTLTVAENESGLCYNSRIR-----YLEKSEVTKRKEISCDDMDFFKS DDEP 175

174 TITWMGCYKIQNENNVIPEGNNLSFLIALISNGNGTVCVVTPENGTFHLTRTLTKVV 233
:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 176 DWMTYCKEKPKMMWSIIQKGNALLIQEVQBEDGANVCELY--EGKL--VRRTTELKV 231

234 VGSPTNAVP-FVHSPPDHAVYEEKRGELLICTVYESFLMDSRENVAMATIDGGKPDPI 292
Db 232 TALLDKPCKPLFPWENOPSVIDVQLGKPLNPCKAFPGFSGESGPITYM--MKGEK--- 286

293 TIDVTYNISISHSRREDTR-----TQILSIKTYSIEDUKSKSYVCHARGAKGEV 341
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 297 ----FIEELAGHIR-EGBEIRLKEHLAGEVELALFDPSVVEADD-ANYTCHEVENRNR- 339

342 AKAAYKOKVAPRYTVETACGFATVLLIVYLIVHYVMLEMVLFRAHFGETDETILD 401
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 340 -KHSHVLRKDDLKIELAGLGAIPLLVLVIVYICVNILEMLFRQHFGADETDMD 398

402 GKXYDIVSYAR-----NAEEEFVLLTLEGVLENFGYKLCIFDRDSLPGANTVE 452
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 399 NKEDYAVLYTFKVDOTLDCCDNPEEQPALLEVLPDVLEKHGYKLIPIERDLISGTME 458

453 AVPDFDIORSRMIVLASPVDTYKTSISMLEKRLGMCONSLAT---KLIIVEYRLEPH 509
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 459 DIIRVEOSRRILLIVDYTLRKWSI--FELSRLNMMLVSGEIKVILLICECLK--- 513

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QY 510 PG-----ILQKESV---SFVSMGKESKSGSKFKALRLALPLR----- 547
DB 514 -GKVNCOEVSLSKRSIKLSLIMKSSKSKSLNSKFKHLYEMPIKCKMLPRCHVLD 572
QY 548 -----SLNASSGWNESCOSQSDISLDHVQRRRSRUKPEPQSS----- 586
DB 573 AEGLFGELOPIPSIMATSTATLVSQADL-----PEFPPSDSMQIRHC 617
QY 587 -----ERAAGSPAPKMSKHKGSATRCVCVCEGENHLRN--KSRAEIH 632
DB 618 CRGKHIEPATLTPVPSLGNH-----TYCNLP/LTLNGQLPLNLTUKTOBEH 666

RESULT 6
US-09-173-151A-2
Sequence 2, Application US/09173151A
Patent No. 6326472

GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
APPLICANT: Debets, Johannes Eduard Maria
APPLICANT: Antonius
APPLICANT: Sana, Theodore R.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,151A
FILING DATE: 14-OCT-1998
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-173-151A-2
Query Match 21.8%; Score 800; DB 4; Length 579;
Best Local Similarity 35.1%; Pred. No. 2.1e-69;
Matches 207; Conservative 96; Mismatches 208; Indels 78; Gaps 24;

QY 1 MTLLCVSLVYFYGLQSD--ASERCDDWGLDTMRQIQVFEDEPAKICPLFEHFLKPNY 58
DB 3 LTL--VSTMLVSTSSPSLSDGICIMSV-D-LTYVALAEPRVKALVYSYIRNY 59
QY 59 STAHSGGLTIWYTRQDRLEPINFLPENRISKQDVLMFRPLTLDNTNTMLRN 118
DB 60 STAQSTGLRLMNY--KNKGDEEPIIF--SEVRMSKEBDSIFWHSAAEDSGFTYCVLN 115
QY 119 TTYCSVAPELLEVQKDS--CNSPMKLPVHLYIEY--IORITCPNDVYPPSSVK 172
DB 116 STYCKVMSLTVVAENESLCTNSRIR-----YLEKSEVTRKEIISCPMDPFKSDOE 169
QY 173 PITYWYGCYKIQNFNNVPIEGMNLSPILALISNNGNYCVVITYPENGRTFHLITRLTVK 232
DB 170 PDVWYKECKPRMRSIITQKNALLIOVQEDGNTYCELY--EGKL--VRRTTEIK 225
QY 233 VVSGPRNAV-PVISHPNDAVVEKEPGEELLIPCTVYFSPIMDSRNEVWTTIDKKPD 291
DB 226 VTALITDKPKPLFPENQPSVIDQKPLNIPCAAFGFGSGSPMIY--MKGEK-- 281
QY 292 ITTIDVTINESISHRTEDTR-----TOLISIKYTSBDUKSYVCHASAKGE 340
DB 282 -----FIEELACHIR-EGEIRILKELHGEKEVALIIPDSVVEALD-ANYTCHVENRNR 334
QY 341 VAKAKVKQVAPRYTVELACFGATVLLVILVHVHVLEWLPFRAHGTDETL 400
DB 335 --KASVLRKKDLYIKLILAGLGIIFLLVLLVITKVIILMLFRQHGADETND 392
QY 401 DKEKDIYVSVAR-----NAEEBEFVLLTLEGVLENEGYKLCIFDRSLPGNT 450
DB 393 DKREDAYLSYTKVQDITDCNPEEBOGFALEVLDPVLEKHGYLKFIERDLISGSAY 452
QY 451 VENAVDEFIORSRMIVLSPDVYTEKSIEMLEFKCWMCONSIAI--KLIVVERPLEH 507
DB 453 MEDLTRVYEOSRRLIIVLPDYILTRGWSI--FELSRILHNNLWGEIIVIIIECTELK- 509
QY 508 PHRG-----ILQKESV---SFVSMGKESKSGSKFKALRLALPLR 547
DB 510 ---GKVNCOEVSLSKRSIKLSLIMKSSKSKSLNSKFKHLYEMPIK 555

RESULT 7
US-09-173-151A-35
Sequence 35, Application US/09173151A
Patent No. 6326472

GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
APPLICANT: Debets, Johannes Eduard Maria
APPLICANT: Antonius
APPLICANT: Sana, Theodore R.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/173,151A
 FILING DATE: 14-OCT-1998
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/065,776
 FILING DATE: 17-NOV-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/078,008
 FILING DATE: 12-MAR-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/081,883
 FILING DATE: 15-APR-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/095,987
 FILING DATE: 10-AUG-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/078,416
 FILING DATE: 18-MAR-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/062,066
 FILING DATE: 15-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Ching, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DX0767X
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650)852-9196
 TELEFAX: (650)496-1200
 INFORMATION FOR SEQ ID NO: 35:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 668 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-173-151A-35

Query Match 20.8%; Score 762.5; DB 4; Length 668;
 Best Local Similarity 29.7%; Pred. No. 1,3e-65;
 Matches 204; Conservative 119; Mismatches 274; Indels 91; Gaps 21;

24 CDDWGLDTRMROIOVFEDEPARIKCPLEFHLKFNYSSTAHSAGLTLIYWTRODRLEPT 83
 3 CTWMSID-IKKYQVLVEBPVAKICALEFYGYRTMYSLAQSHLSIMMYKSSGPDPEPI 61
 84 NFRLEPERSKEDVAFRPTLNDGNYTQMLNTYCSVAPPLVVOXDS--CENSP 141
 62 AF--DGSRMKEEDSWFRPTLQDSGLYACVINNSTYCMKVSISLTVGENDTGLCYNSK 119
 142 MKLPHVHLTYIEG---IORITCPNVGVPPSSVKTPTIYWMGCKLQNFNNVPIEGMNL 197
 120 MK-----YFKELSKSKSKISCRDIEDFLPTREPLIMYKERTKTPRPSIYFKDGL 173
 198 SFLIALISNNNGNYTCVVTYPENGRTFHLTRTLTVKVVGSPKNAVPPVHSPNDH--VVE 255
 174 LIREVREDIDIGNYCEKLY--GCFVVRRTTELVT--APLTDKPLGLYPMESKLTIOE 228
 256 KERGELLICTYVFFSLMDSRNVMTIIOCKRPDI-----TIIDTINESISHSHTED 309
 229 TQJDSANLTCRAFGSGVSPILYMMKGEKLTIEDENRWESDIRI--LKEHLEQ 285
 310 ETRTQILSIKVTSEDKRSYVCHARAKGEVAKAAKQKVPAPRYTVELACFGATVL 369
 286 EVSISL--VDSVERGDL--GNVSCYVENGR--RHASVILMKRELMTVELAGLGLAILL 341
 342 LVLGLTVIYKYKLEIMLFYRNHFGAEELGDNKDYDAVLSYTVKVDPDQNOQTEGEERF 401
 370 LVLVLIVVHYVLEMLFTRAHFGTDETLIDGKEYDIYVSYAR-----NAEEEF 420
 421 VLLTRGLVLENEFGYKLCIPRDSLPGNTEAVFPIQSRBMIVLSDPYTEKSI 480
 402 ALLELPLMELEHNGYKLPIDRDLPTGTYIEDVARCVDSKRLIIVMTPTVYVRKMSI 461
 481 LEFRLGVMCONSIAI--KLIVREYRPLEHPHGLQDK-----SVSEFVSMGEX 528

462 --FELETRLRNMLVTGEIKVILIECEELR-----GIMNYQVEVALKRTIKLITVYKMHGPK 515
 529 SKHSGCKPKKALRALPLR-----SLASGCMNBSGSSQSDISLD 568
 516 CNLNSKFPKRLQYEMPFRIETHEQALDVEGCPFEELQTVSAISMAAATSTALATA 575
 569 HVOR-----RSRLKEPPELOSSERAAGSPAPGMSKHKRGSATRCCTYCEGEN 621
 576 HPLRSTFNTHYSQNRQKHYTRSYEDV--PPTGLPLTISIGNQHTYCNIPMTLNGOR 633
 622 HLNKSRAEIHQPOWETHLCRPQES 649
 634 PQTSSREQNPBEAHTNSAILPLPRET 661

RESULT 8
 US-08-604-333-2
 Sequence 2, Application US/08604333
 Patent No. 5776731

GENERAL INFORMATION:
 APPLICANT: Partec, Patricia et al.
 TITLE OF INVENTION: Receptor Designated 2F1
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101

COMPUTER READABLE FORM:
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Apple 7.1
 SOFTWARE: Microsoft Word, Version 5.1a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/604,333
 FILING DATE: 21-FEB-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Anderson, Kathryn A.
 REGISTRATION NUMBER: 32,172
 REFERENCE/DOCKET NUMBER: 2619
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 231-0644
 TELEX: 756822

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 541 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-604-333-2

Query Match 14.4%; Score 528; DB 1; Length 541;
 Best Local Similarity 30.0%; Pred. No. 8.2e-43;
 Matches 174; Conservative 93; Mismatches 215; Indels 98; Gaps 27;

4 LMCVSLVLYGILQSDASRCDDWGLDTR--OIOVEDEPARIK--CPLEFHLKFNYSST 61
 10 LMLVLIV-----STASC-----TSRPHITVEGEPFYIKHC-----SCSLA 46
 62 HSAGLTL-IWYTRDRODRLEPINFRLPENRISKEDVLMFRPTLNDGNYTQMLRNTT 120
 47 HEIETTKSMYKSSGQEHVE--LNP--SSRIALHDCVLEFVPELNDGSGYFFQKKNY 104
 121 YCSKAFPLEVQ--KDSGFN-----SPMKLPVHLKLYIEGICQIRITCPNMDGVPPSSVKPT 174
 105 Q---KMKNLVIRNKHSGFTERQVYSKIVEVKPF-----QITEN--SYQTQVNST 152
 175 ITWYMGCKYIQNFNNVPE--GNMLSFLIALISNNNGNYTCVVTYPENGRTFHLTRTLTVKY 233


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APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 541 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-173-151A-28

Query Match      14.4%; Score 528; DB 4; Length 541;
Best Local Similarity 30.0%; Pred. No. 8.2e-43;
Matches 174; Conservative 93; Mismatches 215; Indels 98; Gaps 27;

Db      4 LMCVSLYFYGILOSASERCDDMGIDTMR-QIOVFEDPARIK-CPLEFHLKFNSTYA 61
      10 LMWLISV-----STASCS-----TSRPHITVGEPEFLKHC-----SCSLA 46
Oy      62 HSAGLT-ITWTRQDDLEPINFRLPENRISKEDVLMFRPTLNDTGNVLTMLNTT 120
      47 HEIETTKSYKSGSGSEHNE-LNPR-SSSRIALHDCVLEFWPELVNDTSYFFQMKNYT 104
Oy      121 YCSKVAPELVQ--KDSFN---SPMKLPVHKLYIEYGIQRTCPNVGVFPSSVKPT 174
      105 Q---KKLANVIRNKGSCFTEQVTSKIVEKKEF-----QITCEN--SYQTLVNST 152
Oy      175 ITWYMGYKIQNFNNVLP-GMNLSFLIALISNNNGTVCVTVYENGRTHLTTLTKV 233
      153 -SLYKCKKLLLENNKRPYTKKNAEF-----EDGYYSCHPFLHNGKLFNITTFNITI 206
Oy      234 VGSFKNAVPPVHSPNDHYVEKEPGEELLIPCTVYVSFLMDSRNEMWTIDGKKPDIT 293
      207 VEDRSNIVPVLGPKLNHVAEL--GKNVRLNC-----SALINBEDVYIMNGEENGSDPN 260
Oy      294 IDVTINESISHSRTDETRT-----QILSIKVTSEDLKRSYVCHASAKGEVAKAA 345
      261 I-----HEEKEMIMPEGKMHASKVLRIRENIGESNINLVNCTVASTGTDTKSF 311
Oy      346 KVKOK-----VPARYVELACGATVLT---VVLIVVHVWMLMVLYRHAHPGIDE 397
      312 ILVKKAMADIPGHVFT---RGMILAVLIVAVVCLVTVIRVDVLTTRRDE 367
Oy      398 TILGKEYDIIVSAYR-----NAEEEFVLLTLRGVLENEFGYLCIFDRDSLPGQNTVE 452
      368 TLNDGKTYDAFVSTYKGRPRNGEHTFAVEILPRVLEKHYGLCTCFERVVVGGAVVD 427
Oy      453 AVPFQIORSRMIVLSPDYVTEKSIKMLEFKL-GVWKQNSIATKLIVVEYRPLEHPH-- 509
      428 EIHSLIEKSRLLIIVLSKYSMSNEVRYELSGLHEALVERKI--KIILIEPTVLTDTFTL 485

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Oy      510 PGILOLKSQSVFVSWKGEKSKSGSKPMKALRLALPLRSI 549
      486 PSLTKLKKSHRVLKWKADKSLSYNSRPMWOLLVYIMAKTV 525

RESULT 11
US-09-578-178-2
Sequence 2, Application US/09578178
Patent No. 6451760
GENERAL INFORMATION:
APPLICANT: Parnet, Patricia et al.
TITLE OF INVENTION: Receptor Designated 2P1
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/578,178
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/110,618
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2619
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 541 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-578-178-2

Query Match      14.4%; Score 528; DB 4; Length 541;
Best Local Similarity 30.0%; Pred. No. 8.2e-43;
Matches 174; Conservative 93; Mismatches 215; Indels 98; Gaps 27;

Db      4 LMCVSLYFYGILOSASERCDDMGIDTMR-QIOVFEDPARIK-CPLEFHLKFNSTYA 61
      10 LMWLISV-----STASCS-----TSRPHITVGEPEFLKHC-----SCSLA 46
Oy      62 HSAGLT-ITWTRQDDLEPINFRLPENRISKEDVLMFRPTLNDTGNVLTMLNTT 120
      47 HEIETTKSYKSGSGSEHNE-LNPR-SSSRIALHDCVLEFWPELVNDTSYFFQMKNYT 104
Oy      121 YCSKVAPELVQ--KDSFN---SPMKLPVHKLYIEYGIQRTCPNVGVFPSSVKPT 174
      105 Q---KKLANVIRNKGSCFTEQVTSKIVEKKEF-----QITCEN--SYQTLVNST 152
Oy      175 ITWYMGYKIQNFNNVLP-GMNLSFLIALISNNNGTVCVTVYENGRTHLTTLTKV 233
      153 -SLYKCKKLLLENNKRPYTKKNAEF-----EDGYYSCHPFLHNGKLFNITTFNITI 206
Oy      234 VGSFKNAVPPVHSPNDHYVEKEPGEELLIPCTVYVSFLMDSRNEMWTIDGKKPDIT 293
      207 VEDRSNIVPVLGPKLNHVAEL--GKNVRLNC-----SALINBEDVYIMNGEENGSDPN 260
Oy      294 IDVTINESISHSRTDETRT-----QILSIKVTSEDLKRSYVCHASAKGEVAKAA 345

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Db 261 I-----HEEKEMRIMTPEGKMHASKVIRIENIGESNINLVNCTVASTGTDTKSF 311
Qy 346 KVKOK-----VPAARYVELACGATVTL---VVLIVYHYVWLMVLFYRAHPGTDE 397
Db 312 ILVFKADMADIPGHVFT---RGMIIAVLLIVAVCVATVYVAVLVLFYRLTRDR 367
Qy 398 TIIDGKEVDIYVSAR-----NAEEEFVLLTTRGVLENEGYKLCIFEDDSLPGATVE 452
Db 368 TLDGKYDAFVSLKECRENGEHTFAVEILPRVLEKHFYGLCTIFEDDVYGGAVD 427
Qy 453 AVDFIORSRMIVLSPDVYTEKSISMLEPKL-GVMCONSIAKTLIVEXRPLEHPH- 509
Db 428 EIHSLIEKSRRLIIVLSKSYMSNEVREYELSGHEALVERKI--KILIEFTPTDPTFL 465
Qy 510 PGLQKESVSPVSMKEGKSHSGSKFMKALRLALPLRLS 549
Db 486 POSLKLKSHRVLMKADKSLSYNSRFMKQLLYLMPAKTV 525

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RESULT 12

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US-08-996-338-20
; Sequence 20, Application US/08996338
; Patent No. 6087116
; GENERAL INFORMATION:
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: OKURA, Takamori
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,338
; FILING DATE: 22-DEC-1997
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 74,697/1997
; FILING DATE: 12-MAR-1997
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 215,488/1997
; FILING DATE: 28-JUL-1997
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 291,837/1997
; FILING DATE: 09-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TORIGOE-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 521
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-996-338-20

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Query Match 14.2%; Score 520; DB 3; Length 521;
Best Local Similarity 30.5%; Pred. No. 4.7e-42;
Matches 167; Conservative 89; Mismatches 209; Indels 82; Gaps 24;

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Qy 35 IOVEDEPARIK-CPLFEHFLKFNSTASHAGTLT-ITWTRDRDLEIEPINFRLPENRI 92
Db 9 ITVEGEPEFYLLKIC-----SCSLAHEIETTKSMYKSSGSGQEHVE-LNBR-SSSRI 57
Qy 93 SKEKDVLMRPTLLANTGNATCYLKNRTYYSKAPLEVVQ--KDSGFN-----SPMLTPV 146
Db 58 ALADCVLEFMPVRLINDGSGFFQMKRYTO---KMKLANVIRRNKHSCTFERQVYSKIVEV 113
Qy 147 HKLYIEYGIORICPVVDGFPSPVPTITWYMGCYKIQNFNNVIRE-GNNLSFLALIS 205
Db 114 KGF-----QITGEN--STYQTLVNST-SLYKCKKLLBNKNPFIKKNAEF-----E 159
Qy 206 NNGNYTCVVYTPENGRFTFLTRLTIVKVGSPKGAAPPVLIHSPNDHYVEKEPGEELLIP 265
Db 160 DQGYSCVHFLHNKGLFNITTKTFNITIVEDRSNIVPVLLGPLNVAVEL--GQAVRLN 217
Qy 266 CTVYFSPFLMDSRNEVWTTDGGKPPDITTDVTINESISRTEDERT-----OILS 317
Db 218 C-----SALINEEDVVIYMWEGEENGSDPNI-----HEEKEMRIMTPEGKMHASKVIR 264
Qy 318 IKKVTSEDLKRSYVCHASAKGEVAKAKVKOK-----VPAARYVELACGATVTL--- 370
Db 265 IENIGESNINLVNCTVASTGTDTKSFILVRKOMADIPGHVFT---RGMIIAVLLIVA 320
Qy 371 VVLIIVYHYVWLMVLFYRAHFGTETIIDGKEYDIYVSAR-----NAEEEFVLLTL 425
Db 321 VVCLVAVCVIYVDVLFRLHRLRDETLTGCTYDAFVSLKECRENGEHTFAVEIL 380
Qy 426 RGVLENEGYKLCIFEDDSLPGATVEAVDFIORSRMIVLSPDVYTEKSISMLEPKL 485
Db 381 PRVLEKHFYGLCTIFEDDVYGGAVVDEIHSLEKSRRLIIVLSKSYMSNEVREYELSG 440
Qy 486 -GVMCONSIAKTLIVEXRPLEHPH--PGLQKESVSPVSMKEGKSHSGSKFMKALRL 542
Db 441 HEALVERKI--KILIEFTPTDPTFLPSLKLKSHRVLMKADKSLSYNSRFMKQLLY 498
Qy 543 ALPLRLS 549
Db 499 LMPAKTV 505

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RESULT 13

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US-09-173-151A-32
; Sequence 32, Application US/09173151A
; Patent No. 6326472
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Debets, Johannes Eduard Maria
; APPLICANT: Antonius
; APPLICANT: Sana, Theodore R.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: Human Receptor Proteins, Related Reagents and Methods
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/173,151A
; FILING DATE: 14-OCT-1998
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 60/065,776
; FILING DATE: 17-NOV-1997

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE//DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 555 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-173-151A-32

Query Match 13.5%; Score 496; DB 4; Length 555;
Best Local Similarity 26.4%; Pred. No. 1.2e-39;
Matches 155; Conservative 109; Mismatches 230; Indels 94; Gaps 26;

6 CVALYFYGILQSDASERCDMDGLTMKQIVFEDEPARIKCPLEHFLKFNYSASHAG 65
26 CVICNRY-----VINGEPALISCPV-----ITLPMIHS-D 54

66 LTLIWTTRQDRDLDEEPINFLPENRISKEKQVLMFRPTLINDTGNVTOMLNTTYSKV 125
55 YNLTWY--RINGSNM--PITTE-RRARIHQKGLMFTIPALAEISGLYCEVRSLRSKOK 109

126 APLFLEVQKDS--CPNSPKLPHKLYLEIGIQRITCPNVUGY--PPSSVKPTITMYMCY 182
110 IINKVFNQDGLCPNGEMK--YDQIVSANAGKICPDLENFQDEEDINBEIHWYCK 167

183 K--IQFNPNVIREGMN--LSFLIALISNNGNTVCVTPENGRTFHLTLTVKVVSPKN 239
168 SGFLERKLVABEGNALILNVTIQDKGNTCRNVYTMKQYVSTNMLEVYESLKL 227

240 AVPPVHSPNDVHYEKEGSEELLIPCTV---YESFLMDSRNEVWMTIDGKKPDDITIV 296
228 MRPEFIY-PNNNTI-EVELGSHVWMECVSSGVGLL-----PYMQVNDREDD--SPDS 277

297 T-----INESISHRTDETRTQILSIKQVTSSEDLKRSYVCBARAKAEVAKAKVKVKV 351
278 TYRQFTFEEGMPHGIASGTR--FNISEVKIKDYAKYFPGHFIYDSQFTSYIKLEH-- 332

352 PAPRYTELACGATVLLVLLVYVHYVLMELFYRA--HFGTDEITLDGKEYDIYV 409
333 PVQNIKRGILIGGISLILFLILVYIKFIDIVLWRRSCHPLKGVKVDGKIYDAYV 392

410 SYANNAE-----EEEFVLLTRGVLENEFGYKLCIFDRDSLPGGNTVAEVPFIORSRM 464
393 LYPKRRSCCLVSDIFALKILPEVLEKOCGNLFIFGNNDLAGEAIVDTEKIHQSHRV 452

465 IVLVSP-----DYVTEKISIMLEFLGWCONSIATKLIIVETRLP---HHPHIL 513
453 IILVPEPSCGILEDASEKHLAV---YNALIDGCI--KILILEKIEIDYANPESIK 506

514 QLKESVSFVSWKG--EKSKHSGSKFETALRIALPLRSLSASGNNES 558

Db 507 YVQKYGAIRWGTDFSRSHSASTRFMKVKVRYHMPKRGSSSGFHL 554

RESULT 14
US-07-821-716-4
Sequence 4, Application US/07821716
Patent No. 5319071
GENERAL INFORMATION:
APPLICANT: Dower, Steven K.
APPLICANT: March, Carl J.
APPLICANT: Sims, John
TITLE OF INVENTION: Soluble Interleukin-1 Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/821,716
CLASSIFICATION: 530
FILING DATE: 19920114
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 125627
FILING DATE: 25-NOV-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160550
FILING DATE: 25-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 258756
FILING DATE: 13-OCT-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 691551
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wright, Christopher L.
REGISTRATION NUMBER: 31,680
REFERENCE//DOCKET NUMBER: 2001-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 576 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-821-716-4

Query Match 13.2%; Score 484.5; DB 1; Length 576;
Best Local Similarity 25.8%; Pred. No. 1.7e-38;
Matches 153; Conservative 120; Mismatches 225; Indels 95; Gaps 27;

34 QIQVFEDEPARI-----KCPLEHFLKFNYSASHAGTLIWTTRQDRDLDEE 81
21 EIDVCTEYPMQIVLFSVNEIDIRKCPLETPNKNH-----GDTIHW-----KNDSKT 67

82 PINFRLDENRISKEKQVLMFRPTLINDTGNVTGMLRNTTYSKVAFLFLEVQKDS--CFN 139
68 PISAD-RDSRIHQNEHLMVPAKVBSGYCYICIVNSSTYCLAKTKVYVTLNDPGLCY 126

140 SPKLPVHKLYLEIGIQRITCPNVUGY--PPSSVKPTITMYMCYKIQFNPNVIREGMN 197
127 TOATFP-QRLHIA-GDSGLVCPYV-SYFKDENNELPEVCWYKNC-KPLLDNVSFFGVKD 182

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 23, 2003, 08:54:06 ; Search time 45 Seconds

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Title: US-10-061-727-2

Perfect score: 3669

Sequence: 1 MTLWCVSLVYFYLQSDA.....SALALHPTDLSNNDFYLL 687

Scoring table:

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 301932

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2580	70.3	570	9	US-10-215-211-4
3	2327.5	63.4	570	9	US-10-011-548-21
4	1934	52.7	359	9	US-10-215-211-6
5	1930	52.6	910	9	US-09-935-868-28
6	825	22.5	686	9	US-10-011-548-4
7	800	21.8	579	9	US-10-011-548-2
8	762.5	20.8	668	9	US-10-011-548-35
9	528	14.4	541	9	US-10-011-548-28
10	528	14.4	541	10	US-09-981-421-4
11	528	14.4	541	12	US-10-157-447-2
12	496	13.5	555	9	US-10-011-548-32
13	484.5	13.2	576	9	US-10-011-548-30
14	484.5	13.2	576	10	US-09-731-175-4
15	479	13.1	537	9	US-10-011-548-29
16	479	13.1	537	12	US-10-157-447-4
17	478	13.0	567	9	US-10-011-548-24
18	478	13.0	567	9	US-10-004-633-39
19	478	13.0	567	10	US-09-899-980A-7

20	471.5	12.9	599	9	US-09-731-449-2	Sequence 2, Appli
21	471.5	12.9	599	9	US-10-212-287-7	Sequence 7, Appli
22	471.5	12.9	599	9	US-10-011-548-10	Sequence 10, Appli
23	471.5	12.9	599	10	US-09-981-421-2	Sequence 2, Appli
24	471	12.8	580	9	US-09-731-449-8	Sequence 8, Appli
25	463.5	12.6	556	10	US-09-899-980A-8	Sequence 8, Appli
26	457	12.5	561	9	US-10-011-548-23	Sequence 23, Appli
27	457	12.5	561	10	US-09-775-046-15	Sequence 15, Appli
28	446	12.2	614	9	US-10-212-287-2	Sequence 2, Appli
29	446	12.2	614	9	US-10-011-548-16	Sequence 16, Appli
30	445	12.1	610	9	US-10-011-548-14	Sequence 14, Appli
31	444.5	12.1	562	9	US-10-011-548-22	Sequence 22, Appli
32	444.5	12.1	562	10	US-09-775-046-13	Sequence 13, Appli
33	436	11.9	467	9	US-10-011-548-8	Sequence 8, Appli
34	424.5	11.6	569	9	US-10-011-548-31	Sequence 31, Appli
35	424.5	11.6	569	10	US-09-840-707A-3	Sequence 3, Appli
36	424.5	11.6	569	10	US-09-731-175-2	Sequence 3, Appli
37	414	11.3	486	9	US-10-011-548-20	Sequence 20, Appli
38	413.5	11.3	481	10	US-09-764-853-655	Sequence 655, App
39	392	10.7	70	10	US-09-864-761-48704	Sequence 48704, A
40	314	8.6	410	9	US-10-011-548-27	Sequence 27, Appli
41	314	8.6	410	9	US-10-199-209-13	Sequence 13, Appli
42	290.5	7.9	217	9	US-09-731-449-11	Sequence 11, Appli
43	252	6.9	398	9	US-10-215-211-2	Sequence 2, Appli
44	252	6.9	398	9	US-10-011-548-26	Sequence 26, Appli
45	252	6.9	398	9	US-10-199-209-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-011-548-36
Sequence 36, Application US/10011548
Publication No. US20030055218A1
GENERAL INFORMATION:
APPLICANT: Tibets, Jacqueline C.
Antoniou
Sana, Theodore R.
Bazan, J. Fernando
Kastelein, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,548
FILING DATE: 22-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/173,151
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-Nov-1997
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-Mar-1998
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-Apr-1998
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-Aug-1998
APPLICATION NUMBER: US 60/078,416

```

;
; FILING DATE: 18-MAR-1998
; APPLICATION NUMBER: US 60/062,066
; FILING DATE: 15-OCT-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Chang, Edwin P.
;   REGISTRATION NUMBER: 34,090
;   REFERENCE/DOCKET NUMBER: DX0767X
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (650) 852-9196
;   TELEFAX: (650) 496-1200
; INFORMATION FOR SEQ ID NO: 36:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 570 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: No.
;     TOPOLOGY: Linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-011-548-36

Query Match          70.5%; Score 2586; DB 9; Length 570;
Best Local Similarity 85.3%; Pred. No. 4.2e-200;
Matches 488; Conservative 35; Mismatches 37; Indels 12; Gaps 4;

QY 1 MTLIMCVSLYFYGIIQSDASERCDMDGLDTMRQIQVFEDPARIKCPLEHFLKFNYST 60
DB 1 MTLIMCVSLYFYGIIQSDASERCDMDGLDTMRQIQVFEDPARIKCPLEHFLKFNYST 60
QY 61 AHSAGLTLIWYTRQDRDLSEPIINFRLPENRISKEDVLMFRPTLNDTGNITCMLNNT 120
DB 61 AHSAGLTLIWYTRQDRDLSEPIINFRLPENRISKEDVLMFRPTLNDTGNITCMLNNT 120
QY 121 YCSKVAPELVQKDSGFNSPMKLPVHKLYIEGIIQITCPNDVGFPPSSVKPPTITWYG 180
DB 121 YCSKVAPELVQKDSGFNSPMKLPVHKLYIEGIIQITCPNDVGFPPSSVKPPTITWYG 180
QY 121 YCSKVAPELVQKDSGFNSPMKLPVHKLYIEGIIQITCPNDVGFPPSSVKPPTITWYG 180
DB 121 YCSKVAPELVQKDSGFNSPMKLPVHKLYIEGIIQITCPNDVGFPPSSVKPPTITWYG 180
QY 181 CYKIQNFNNVYIPSGMNLSPFLIALISNNNGNTCVVTPENGRTHLRTLLTVKVGSPKNA 240
DB 181 CYKIQNFNNVYIPSGMNLSPFLIALISNNNGNTCVVTPENGRTHLRTLLTVKVGSPKNA 240
QY 181 CYKIQNFNNVYIPSGMNLSPFLIALISNNNGNTCVVTPENGRTHLRTLLTVKVGSPKNA 240
DB 181 CYKIQNFNNVYIPSGMNLSPFLIALISNNNGNTCVVTPENGRTHLRTLLTVKVGSPKNA 240
QY 241 VPPVISHPNHVVYKKEPGEELIPCTVYFSLMDSRNEVMTIDGKKPDDITIDVTINE 300
DB 241 VPPVISHPNHVVYKKEPGEELIPCTVYFSLMDSRNEVMTIDGKKPDDITIDVTINE 300
QY 241 VPPVISHPNHVVYKKEPGEELIPCTVYFSLMDSRNEVMTIDGKKPDDITIDVTINE 300
DB 241 VPPVISHPNHVVYKKEPGEELIPCTVYFSLMDSRNEVMTIDGKKPDDITIDVTINE 300
QY 301 SISHSRTEDETRQIISIKKVTSEDLKRSYVCHARSAKGEVAAKAVKQVAPRYVEL 360
DB 301 SISHSRTEDETRQIISIKKVTSEDLKRSYVCHARSAKGEVAAKAVKQVAPRYVEL 360
QY 301 SISHSRTEDETRQIISIKKVTSEDLKRSYVCHARSAKGEVAAKAVKQVAPRYVEL 360
DB 301 SISHSRTEDETRQIISIKKVTSEDLKRSYVCHARSAKGEVAAKAVKQVAPRYVEL 360
QY 361 ACAGGATVLLVLLIYVHYVYMLEMVLFYRAHFGTDETLIDGKEYDIYVSAYARAAEEEF 420
DB 361 ACAGGATVLLVLLIYVHYVYMLEMVLFYRAHFGTDETLIDGKEYDIYVSAYARAAEEEF 420
QY 361 ACAGGATVLLVLLIYVHYVYMLEMVLFYRAHFGTDETLIDGKEYDIYVSAYARAAEEEF 420
DB 361 ACAGGATVLLVLLIYVHYVYMLEMVLFYRAHFGTDETLIDGKEYDIYVSAYARAAEEEF 420
QY 421 VLLTLRGVLENERGYKLCIFDRDSLPGAGNTVEAVFDFIORSRMIVVLSPDYVTEKISIM 480
DB 421 VLLTLRGVLENERGYKLCIFDRDSLPGAGNTVEAVFDFIORSRMIVVLSPDYVTEKISIM 480
QY 421 VLLTLRGVLENERGYKLCIFDRDSLPGAGNTVEAVFDFIORSRMIVVLSPDYVTEKISIM 480
DB 421 VLLTLRGVLENERGYKLCIFDRDSLPGAGNTVEAVFDFIORSRMIVVLSPDYVTEKISIM 480
QY 481 LEFLGLGMCNSTATK---LIYVERPLLEHPHPIQLKES---VSFVSKGKSKSHSG 533
DB 481 LEFLGLGMCNSTATK---LIYVERPLLEHPHPIQLKES---VSFVSKGKSKSHSG 533
QY 481 LEFLGLGMCNSTATK---LIYVERPLLEHPHPIQLKES---VSFVSKGKSKSHSG 533
DB 481 LEFLGLGMCNSTATK---LIYVERPLLEHPHPIQLKES---VSFVSKGKSKSHSG 533
QY 534 SKFWKALRLALPLRSLASAGMNSCQSOSDI 565
DB 534 SKFWKALRLALPLRSLASAGMNSCQSOSDI 565
QY 536 GRFWKQLQVAMPVKKSPRRSSSDDEGLSYSSL 567
DB 536 GRFWKQLQVAMPVKKSPRRSSSDDEGLSYSSL 567

RESULT 2
US-10-215-211-4
; Sequence 4, Application US/10215211
; Publication No. US20030049255A1
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Smith, Dirk E.
; TITLE OF INVENTION: INTERLEUKIN-1 RECEPTORS IN THE TREATMENT OF DISEASES
```

```

; FILE REFERENCE: 3321-A
; CURRENT APPLICATION NUMBER: US/10/215,211
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US 60/310,789
; PRIOR FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-215-211-4

Query Match          70.3%; Score 2580; DB 9; Length 570;
Best Local Similarity 85.6%; Pred. No. 1.3e-199;
Matches 487; Conservative 31; Mismatches 45; Indels 6; Gaps 3;

QY 1 MTLIMCVSLYFYGIIQSDASERCDMDGLDTMRQIQVFEDPARIKCPLEHFLKFNYST 60
DB 1 MTLIMCVSLYFYGIIQSDASERCDMDGLDTMRQIQVFEDPARIKCPLEHFLKFNYST 60
QY 61 AHSAGLTLIWYTRQDRDLSEPIINFRLPENRISKEDVLMFRPTLNDTGNITCMLNNT 120
DB 61 AHSAGLTLIWYTRQDRDLSEPIINFRLPENRISKEDVLMFRPTLNDTGNITCMLNNT 120
QY 121 YCSKVAPELVQKDSGFNSPMKLPVHKLYIEGIIQITCPNDVGFPPSSVKPPTITWYG 180
DB 121 YCSKVAPELVQKDSGFNSPMKLPVHKLYIEGIIQITCPNDVGFPPSSVKPPTITWYG 180
QY 121 YCSKVAPELVQKDSGFNSPMKLPVHKLYIEGIIQITCPNDVGFPPSSVKPPTITWYG 180
DB 121 YCSKVAPELVQKDSGFNSPMKLPVHKLYIEGIIQITCPNDVGFPPSSVKPPTITWYG 180
QY 181 CYKIQNFNNVYIPSGMNLSPFLIALISNNNGNTCVVTPENGRTHLRTLLTVKVGSPKNA 240
DB 181 CYKIQNFNNVYIPSGMNLSPFLIALISNNNGNTCVVTPENGRTHLRTLLTVKVGSPKNA 240
QY 181 CYKIQNFNNVYIPSGMNLSPFLIALISNNNGNTCVVTPENGRTHLRTLLTVKVGSPKNA 240
DB 181 CYKIQNFNNVYIPSGMNLSPFLIALISNNNGNTCVVTPENGRTHLRTLLTVKVGSPKNA 240
QY 241 VPPVISHPNHVVYKKEPGEELIPCTVYFSLMDSRNEVMTIDGKKPDDITIDVTINE 300
DB 241 VPPVISHPNHVVYKKEPGEELIPCTVYFSLMDSRNEVMTIDGKKPDDITIDVTINE 300
QY 241 VPPVISHPNHVVYKKEPGEELIPCTVYFSLMDSRNEVMTIDGKKPDDITIDVTINE 300
DB 241 VPPVISHPNHVVYKKEPGEELIPCTVYFSLMDSRNEVMTIDGKKPDDITIDVTINE 300
QY 301 SISHSRTEDETRQIISIKKVTSEDLKRSYVCHARSAKGEVAAKAVKQVAPRYVEL 360
DB 301 SISHSRTEDETRQIISIKKVTSEDLKRSYVCHARSAKGEVAAKAVKQVAPRYVEL 360
QY 301 SISHSRTEDETRQIISIKKVTSEDLKRSYVCHARSAKGEVAAKAVKQVAPRYVEL 360
DB 301 SISHSRTEDETRQIISIKKVTSEDLKRSYVCHARSAKGEVAAKAVKQVAPRYVEL 360
QY 361 ACAGGATVLLVLLIYVHYVYMLEMVLFYRAHFGTDETLIDGKEYDIYVSAYARAAEEEF 420
DB 361 ACAGGATVLLVLLIYVHYVYMLEMVLFYRAHFGTDETLIDGKEYDIYVSAYARAAEEEF 420
QY 361 ACAGGATVLLVLLIYVHYVYMLEMVLFYRAHFGTDETLIDGKEYDIYVSAYARAAEEEF 420
DB 361 ACAGGATVLLVLLIYVHYVYMLEMVLFYRAHFGTDETLIDGKEYDIYVSAYARAAEEEF 420
QY 421 VLLTLRGVLENERGYKLCIFDRDSLPGAGNTVEAVFDFIORSRMIVVLSPDYVTEKISIM 480
DB 421 VLLTLRGVLENERGYKLCIFDRDSLPGAGNTVEAVFDFIORSRMIVVLSPDYVTEKISIM 480
QY 421 VLLTLRGVLENERGYKLCIFDRDSLPGAGNTVEAVFDFIORSRMIVVLSPDYVTEKISIM 480
DB 421 VLLTLRGVLENERGYKLCIFDRDSLPGAGNTVEAVFDFIORSRMIVVLSPDYVTEKISIM 480
QY 481 LEFLGLGMCNSTATK---LIYVERPLLEHPHPIQLKES---VSFVSKGKSKSHSG 536
DB 481 LEFLGLGMCNSTATK---LIYVERPLLEHPHPIQLKES---VSFVSKGKSKSHSG 536
QY 481 LEFLGLGMCNSTATK---LIYVERPLLEHPHPIQLKES---VSFVSKGKSKSHSG 536
DB 481 LEFLGLGMCNSTATK---LIYVERPLLEHPHPIQLKES---VSFVSKGKSKSHSG 536
QY 537 WKALRLALPLRSLASAGMNSCQSOSDI 565
DB 537 WKALRLALPLRSLASAGMNSCQSOSDI 565
QY 539 WKQLQVAMPVKKSPRRSSSDDEGLSYSSL 567
DB 539 WKQLQVAMPVKKSPRRSSSDDEGLSYSSL 567

RESULT 3
US-10-011-548-21
; Sequence 21, Application US/10011548
; Publication No. US20030055218A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Debets, Johannes Eduard Maria
; APPLICANT: Antonius
; APPLICANT: Sana, Theodore R.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kaestlein, Robert A.
; TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: DMAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,548
FILING DATE: 22-OCT-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/173,151
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-9196
TELEFAX: (650) 496-1200
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 570 amino acids
TYPE: amino acid
STRANDEDNESS: No. US2003005218A1 Relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
-10-011-548-21
Query Match 63.4%; Score 2327.5; DB 9; Length 570;
Best Local Similarity 75.9%; Pred. No. 2,9e-179;
Matches 429; Conservative 66; Mismatches 55; Indels 15; Gaps 5;
QY 1 MTLWCVSLYFYGIQSDASERCDWGLDTMRQIOVFEDPARIKCPLEHFLKENYST 60
DB 1 MGLMTWMLSLFYGILQSDASERCDWGLDTMRQIOVFEDPARIKCPLEHFLKENYST 60
QY 61 AHSAGTLTWMYTRORDLEBPINFLPENRISKEKDVLMFRPTLNDGNTYCMRLNTT 120
DB 61 AHSAGTLTWMYTRORDLEBPINFLPENRISKEKDVLMFRPTLNDGNTYCMRLNTT 120
QY 121 YCSKVAFLPELVQKSCFNSPMKLPHKLYIEGIORITCPNVGYPSSVKFTITWYG 180
DB 121 YCSKVAFLPELVQKSCFNSPMKLPHKLYIEGIORITCPNVGYPSSVKFTITWYG 180
QY 181 CYKIQNFNNVIEGKMLSLIALISNNGNTCVVYTPENGRTFHLTRITLVKVGSPKNA 240
DB 181 CYKIQNFNNVIEGKMLSLIALISNNGNTCVVYTPENGRTFHLTRITLVKVGSPKNA 240
QY 241 VPPVHSPNDHVYKEPEBELIPCTVYFSFLMDSRNEVMTTIDKKPDITIDVTINE 300
DB 241 VPPVHSPNDHVYKEPEBELIPCTVYFSFLMDSRNEVMTTIDKKPDITIDVTINE 300
QY 301 SISHSRTEDETRTQILSIKVTSEDLKRSYVCHARSAGEVAKAAVKOKVPAARYTVE 360
DB 301 SISHSRTEDETRTQILSIKVTSEDLKRSYVCHARSAGEVAKAAVKOKVPAARYTVE 360

DB 301 SVSYSTEDETRTQILSIKVTSEDLKRSYVCHARSAGEVAKAAVKOKVPAARYTVE 360
QY 361 ACQFGATVLLVYLIVYVHYVWLEWLFYRAHGTDETLIDGKEDYIYSYARNAEEEF 420
DB 361 ACQFGATVLLVYLIVYVHYVWLEWLFYRAHGTDETLIDGKEDYIYSYARNAEEEF 420
QY 421 VLLTRGVLENFEGYKLCIFDRDSLPGNTVEAVDPFIORSRMIVLSPDYTEKSISM 480
DB 421 VLLTRGVLENFEGYKLCIFDRDSLPGNTVEAVDPFIORSRMIVLSPDYTEKSISM 480
QY 481 LEPKGLVWMCNSIATK---LIVEYRPLEHPRHGLQKES---VSFWSKKEKSKHSG 533
DB 481 LEPKGLVWMCNSIATK---LIVEYRPLEHPRHGLQKES---VSFWSKKEKSKHSG 533
QY 534 SKFWALRLALPLRSLSSASSGNES 558
DB 534 GRFWKQLQVAMPVK--SPRWSN 557
RESULT 4
US-10-215-211-6
Sequence 6, Application US/10215211
Publication No. US20030049255A1
GENERAL INFORMATION:
APPLICANT: Sims, John E.
TITLE OF INVENTION: INTERLEUKIN-1 RECEPTORS IN THE TREATMENT OF DISEASES
FILE REFERENCE: 3321-A
CURRENT APPLICATION NUMBER: US/10/215,211
CURRENT FILING DATE: 2002-08-07
PRIOR APPLICATION NUMBER: US 60/310,789
PRIOR FILING DATE: 2001-08-07
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 359
TYPE: PRT
ORGANISM: Homo sapiens
US-10-215-211-6
Query Match 52.7%; Score 1934; DB 9; Length 359;
Best Local Similarity 99.7%; Pred. No. 7,6e-148;
Matches 358; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MTLWCVSLYFYGIQSDASERCDWGLDTMRQIOVFEDPARIKCPLEHFLKENYST 60
DB 1 MTLWCVSLYFYGIQSDASERCDWGLDTMRQIOVFEDPARIKCPLEHFLKENYST 60
QY 61 AHSAGTLTWMYTRORDLEBPINFLPENRISKEKDVLMFRPTLNDGNTYCMRLNTT 120
DB 61 AHSAGTLTWMYTRORDLEBPINFLPENRISKEKDVLMFRPTLNDGNTYCMRLNTT 120
QY 121 YCSKVAFLPELVQKSCFNSPMKLPHKLYIEGIORITCPNVGYPSSVKFTITWYG 180
DB 121 YCSKVAFLPELVQKSCFNSPMKLPHKLYIEGIORITCPNVGYPSSVKFTITWYG 180
QY 181 CYKIQNFNNVIEGKMLSLIALISNNGNTCVVYTPENGRTFHLTRITLVKVGSPKNA 240
DB 181 CYKIQNFNNVIEGKMLSLIALISNNGNTCVVYTPENGRTFHLTRITLVKVGSPKNA 240
QY 241 VPPVHSPNDHVYKEPEBELIPCTVYFSFLMDSRNEVMTTIDKKPDITIDVTINE 300
DB 241 VPPVHSPNDHVYKEPEBELIPCTVYFSFLMDSRNEVMTTIDKKPDITIDVTINE 300
QY 301 SISHSRTEDETRTQILSIKVTSEDLKRSYVCHARSAGEVAKAAVKOKVPAARYTVE 359
DB 301 SISHSRTEDETRTQILSIKVTSEDLKRSYVCHARSAGEVAKAAVKOKVPAARYTVE 359
RESULT 5
US-09-935-868-28
Sequence 28, Application US/09935868
Patent No. US20020164690A1

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; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 910
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-935-866-28

Query Match          52.6%; Score 1930; DB 9; Length 910;
Best Local Similarity 99.7%; Pred. No. 6,3e-147;
Matches 357; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTLKCVSLIYFYGILOSASERCDMDGLTMRQIQVPEDEPARIKPLFEHFLKENVST 60
    |||||
    1 MVLKCVSLIYFYGILOSASERCDMDGLTMRQIQVPEDEPARIKPLFEHFLKENVST 60

QY 61 AHSAGLTLIWMYTRQDDEEPINFRLEPNRISKEKDVLMFRPLTNDGTGNTMLANTT 120
    |||||
    61 AHSAGLTLIWMYTRQDDEEPINFRLEPNRISKEKDVLMFRPLTNDGTGNTMLANTT 120

QY 121 YCSKVAFPLEVVOKDS-CFNSPMKLPVHKLYIEYGIQRTCPNVDSYFPSSVKPTITWYMG 180
    |||||
    121 YCSKVAFPLEVVOKDS-CFNSPMKLPVHKLYIEYGIQRTCPNVDSYFPSSVKPTITWYMG 180

QY 121 YCSKVAFPLEVVOKDS-CFNSPMKLPVHKLYIEYGIQRTCPNVDSYFPSSVKPTITWYMG 180
    |||||
    121 YCSKVAFPLEVVOKDS-CFNSPMKLPVHKLYIEYGIQRTCPNVDSYFPSSVKPTITWYMG 180

QY 181 CYKIQNFNNVYIPGGMNLSPLIALISNNGNNTCVVTPYENGRTFHLTTLTKVGVSPRNA 240
    |||||
    181 CYKIQNFNNVYIPGGMNLSPLIALISNNGNNTCVVTPYENGRTFHLTTLTKVGVSPRNA 240

QY 181 CYKIQNFNNVYIPGGMNLSPLIALISNNGNNTCVVTPYENGRTFHLTTLTKVGVSPRNA 240
    |||||
    181 CYKIQNFNNVYIPGGMNLSPLIALISNNGNNTCVVTPYENGRTFHLTTLTKVGVSPRNA 240

QY 241 VPPVHSPNDHVYKEKRGEBLLPCTVYFSFLMDSRNEVMTIDGKKPDDITIDVTINE 300
    |||||
    241 VPPVHSPNDHVYKEKRGEBLLPCTVYFSFLMDSRNEVMTIDGKKPDDITIDVTINE 300

QY 241 VPPVHSPNDHVYKEKRGEBLLPCTVYFSFLMDSRNEVMTIDGKKPDDITIDVTINE 300
    |||||
    241 VPPVHSPNDHVYKEKRGEBLLPCTVYFSFLMDSRNEVMTIDGKKPDDITIDVTINE 300

QY 301 SISHSRTEDTRQIILSIKVTSEDLKRSYVCHARSAGKGVAKAKVAKQKVPARITY 358
    |||||
    301 SISHSRTEDTRQIILSIKVTSEDLKRSYVCHARSAGKGVAKAKVAKQKVPARITY 358

QY 301 SISHSRTEDTRQIILSIKVTSEDLKRSYVCHARSAGKGVAKAKVAKQKVPARITY 358
    |||||
    301 SISHSRTEDTRQIILSIKVTSEDLKRSYVCHARSAGKGVAKAKVAKQKVPARITY 358

RESULT 6
US-10-011-548-4
; Sequence 4, Application US/10011548
; Publication No. US20030055218A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; Debets, Johannes Eduard Maria
; Antonius
; Sana, Theodore R.
; Bazan, J. Fernando
; Kastelen, Robert A.
; TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and
; Methods
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSER: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/011,548

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; FILING DATE: 22-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/173,151
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/065,776
; FILING DATE: 17-Nov-1997
; APPLICATION NUMBER: US 60/078,008
; FILING DATE: 12-Mar-1998
; APPLICATION NUMBER: US 60/081,883
; FILING DATE: 15-Apr-1998
; APPLICATION NUMBER: US 60/095,987
; FILING DATE: 10-Aug-1998
; APPLICATION NUMBER: US 60/078,416
; FILING DATE: 18-Mar-1998
; APPLICATION NUMBER: US 60/062,066
; FILING DATE: 15-Oct-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0767X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 852-9196
; TELEFAX: (650) 496-1200
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 686 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-011-548-4

Query Match          22.5%; Score 825; DB 9; Length 686;
Best Local Similarity 31.9%; Pred. No. 4,9e-58;
Matches 228; Conservative 106; Mismatches 244; Indels 136; Gaps 27;

QY 1 MTLKCVSLIYFYGILOSASERCDMDGLTMRQIQVPEDEPARIKPLFEHFLKENVST 59
    |||||
    7 LALVCSVSTNLKMWKRSVDCIDMSVD-LKTYMALAGEVRYKCALFYSTIRNTYS 65

QY 60 TASHAGLTLIWMYTRQDDEEPINFRLEPNRISKEKDVLMFRPLTNDGTGNTMLANTT 119
    |||||
    66 TASHAGLTLIWMYTRQDDEEPINFRLEPNRISKEKDVLMFRPLTNDGTGNTMLANTT 119

QY 66 TASHAGLTLIWMYTRQDDEEPINFRLEPNRISKEKDVLMFRPLTNDGTGNTMLANTT 119
    |||||
    66 TASHAGLTLIWMYTRQDDEEPINFRLEPNRISKEKDVLMFRPLTNDGTGNTMLANTT 119

QY 120 TYCSKVAFPLEVVOKDS-CFNSPMKLPVHKLYIEYGIQRTCPNVDSYFPSSVKP 173
    |||||
    122 TYCSKVAFPLEVVOKDS-CFNSPMKLPVHKLYIEYGIQRTCPNVDSYFPSSVKP 173

QY 122 TYCSKVAFPLEVVOKDS-CFNSPMKLPVHKLYIEYGIQRTCPNVDSYFPSSVKP 173
    |||||
    122 TYCSKVAFPLEVVOKDS-CFNSPMKLPVHKLYIEYGIQRTCPNVDSYFPSSVKP 173

QY 174 TITWYMGCTYKIQNFNNVYIPGGMNLSPLIALISNNGNNTCVVTPYENGRTFHLTTLTKV 233
    |||||
    176 DVVWYKECKRQWRSIITQGNALLIQEVOEDGNTYCEKLT--EKKL--VRRTELKV 231

QY 176 DVVWYKECKRQWRSIITQGNALLIQEVOEDGNTYCEKLT--EKKL--VRRTELKV 231
    |||||
    176 DVVWYKECKRQWRSIITQGNALLIQEVOEDGNTYCEKLT--EKKL--VRRTELKV 231

QY 234 VGSPPKAVP-PVHSPNDHVYKEKRGEBLLPCTVYFSFLMDSRNEVMTIDGKKPDDI 292
    |||||
    232 TALLTDKPPKPLFPMKQPSVIDVQGLKPLNTFCCKAFGSGSGSPITW-MGGR----- 286

QY 232 TALLTDKPPKPLFPMKQPSVIDVQGLKPLNTFCCKAFGSGSGSPITW-MGGR----- 286
    |||||
    232 TALLTDKPPKPLFPMKQPSVIDVQGLKPLNTFCCKAFGSGSGSPITW-MGGR----- 286

QY 293 TIDVTINESISHSRTEDTR-----TQILSIKVTSEDLKRSYVCHARSAGKGV 341
    |||||
    287 -----FIELAGHIR-BGEIRLKEHLEKEVEELALIFDSVVEADL--ANYTCHVENRGR- 339

QY 287 -----FIELAGHIR-BGEIRLKEHLEKEVEELALIFDSVVEADL--ANYTCHVENRGR- 339
    |||||
    287 -----FIELAGHIR-BGEIRLKEHLEKEVEELALIFDSVVEADL--ANYTCHVENRGR- 339

QY 342 AKAKAVQKVPARITYVELACGFATVLLVLLVYHVVMLEVMVLYRAPHGDETIID 401
    |||||
    340 -KASVILARKKDLIYKIELAGGJALFLLVLLVVIYKCNIELMLFYRQHPGADRDND 398

QY 340 -KASVILARKKDLIYKIELAGGJALFLLVLLVVIYKCNIELMLFYRQHPGADRDND 398
    |||||
    340 -KASVILARKKDLIYKIELAGGJALFLLVLLVVIYKCNIELMLFYRQHPGADRDND 398

QY 402 GKEVDIVSYAR-----NAEEEFVLLTLRGVLENFEGYKLCIFDDSLPGGNTVE 452
    |||||
    399 NKEVDIVSYAR-----NAEEEFVLLTLRGVLENFEGYKLCIFDDSLPGGNTVE 452

QY 399 NKEVDIVSYAR-----NAEEEFVLLTLRGVLENFEGYKLCIFDDSLPGGNTVE 452
    |||||
    399 NKEVDIVSYAR-----NAEEEFVLLTLRGVLENFEGYKLCIFDDSLPGGNTVE 452

QY 453 AVPDFIORSRMIVLSPDVYTESISMLEFKLGWMCNSIAT--KLIVVEYRPLEPH 509
    |||||
    459 DLTRYVQSRRLLIIVLPDYLIRGWSI--FELESRLHNLVSGEIVKIVILICTELK--- 513

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QY 510 PG-----ILOQKESV---SFEVSWKGEKSKHSGKFWKALRLALPLR----- 547
Db 514 -GKNCQEVESLKRISIKLSTIKWKSGSKSLKNSKFWKHLVYEMPIKKEMLPRCHVLD 572
QY 548 -----SLSASSGNNESCSQSDISLHVQRRRRLKEPELQSS----- 586
Db 573 AEQGLPELOPIPIAMTSTATVLSQADL-----PEFHSDSMQIRHC 617
QY 587 -----ERAGSPAPGMSKGRGSSATRCCTVYCGENHLRN--KSRAEIH 632
Db 618 CRGKHEIPATTLFVPSLGNH-----TYCNLPILLANGQLPLNNYTLKDTQEPH 666

RESULT 7
US-10-011-548-2
; Sequence 2, Application US/10011548
; Publication No. US20030055218A1
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
Antonijs
Sana, Theodore R.
Bazan, J. Fernando
Kastelein, Robert A.
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,548
FILING DATE: 22-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/173,151
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-9196
TELEFAX: (650) 496-1200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 amino acids
* TYPE: amino acid
* TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-011-548-2

Query Match 21.8%; Score 800; DB 9; Length 579;
Best Local Similarity 35.1%; Pred. No. 4e-56;
Matches 207; Conservativity 96; Mismatches 208; Indels 78; Gaps 24;

QY 1 MTLKCVSLYFYGILOSD--ASERCDWGLDMROIQVFEDEPARIKCPLEHFLKFN 58
Db 3 LTLF--VSTMLTVSYSSDPLSDVDCIDMSVD--LKYMALAGSPVAVKCALFYSYIRTN 59
QY 59 STAHAGTLIMWTRODPLPEPILRLPENNISEKVLMPRLTNDNTGYTCMLN 118
Db 60 STAOSTGLRLMWY--KRGDLEPILF--SEVMSKEBDSIMFSAADAQSGFTVCLRN 115
QY 119 TTYCSKVAFPLEVYOKDS--CFNSPMKLPVHKLYIEYG---IQRITCPVNDYFPSSVK 172
Db 116 STYCMKYSMLTYAENESGICVNSRIR-----YLEKSVTRKEIKSCPMDFKSDQE 169
QY 173 PTTWTCYKIQNFNNVPEGNLSFLALISNNNYTCVITYPENGRTEHLTRLITVK 232
Db 170 PDVWVYKECKPKMWRSLIQGNALLIQVEQEDGNYTCELRY--EGKL--VRRITELK 225
QY 233 VNSGPKNAVP-PIHSPNDHVYKEKRGELLICTVYSEFLMDSRNEVWMTIDGKKPD 291
Db 226 VTALLTDKPKPLPPEMNOFSVIDVQIGKPLNPKCAFSGSGSGPMIYW-MKGEK-- 281
QY 292 ITLDVTINESISRTEDETR-----TOISIKVTSBDLKRSYVCHARSAKGE 340
Db 282 -----FIEELAGHIR-BGEIRLKEHGEKVEALALIFDSVENDL-ANTTCVENNGR 334
QY 341 VAKAAKVKQVPAPRYTVELACFGATVLVILVYVHYVLMEMLYFAHFGTDETL 400
Db 335 --KHAATLAKKOLIKYKELAGIGAIPLLVLVVIYKYNELMLFYRQHGADBTND 392
QY 401 DGEKYDIYSYAR-----NAEEEFVLTLRGYLENEBEGYKLCIFPRDPLPGANT- 450
Db 393 DNKEYAYALSYTVQDDPTLDCDNPBEEQFALFVPLEKHYGYKLFIPERDIPSSAY 452
QY 451 VEAVFPDIORSRMIVLSPDYTEKSISSLBEPKLGVMCONSIAT--KLIVVEYRLEH 507
Db 453 MEDTTRYEQSRULIVLTDTYLIRGWSI--FELSRRLNMLVSGEIKVILIECTELK- 509
QY 508 PHRG-----ILOQKESV---SFEVSWKGEKSKHSGKFWKALRLALPLR 547
Db 510 ---GKNCQEVESLKRISIKLSTIKWKSGSKSLKNSKFWKHLVYEMPIK 555

RESULT 8
US-10-011-548-35
; Sequence 35, Application US/10011548
; Publication No. US20030055218A1
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
Antonijs
Sana, Theodore R.
Bazan, J. Fernando
Kastelein, Robert A.
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

Thu May 1 09:36:19 2003

us-10-061-727-2.rapb

Page 6

APPLICATION NUMBER: US/10/011,548
FILING DATE: 22-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/117,151
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
APPLICATION NUMBER: US 60/078,411
FILING DATE: 18-MAR-1998
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Chang, Edwin P.
REGISTRATION NUMBER: 34,050
REFERENCE/DOCKET NUMBER: DX0676X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 668 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-10-011-548-35.

Query Match	20.8%;	Score 762.5;	DB 9;	Length 668;
Best Local Similarity	29.7%;	Pred. No. 5.2e-53;		
Matches 204;	Conservative 119;	Mismatches 274;	Indels 91;	Gaps 21

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0Y 24 CDGMDLMBROQVEDBPRAIKCPLFENHFKFNYSSTAHSGILTIWMTRODRLAEPI 83
Db 3 CTDMSID-IKTIQVLYGEPVAKALFGYIRITMSILOSAGLSLMTKSSGCPDFEPI 61
0Y 84 NFRLPEBNIISKEKDLWMPRLTLNDYNTGMLRNTTYCSKVAEPPELVOKDS--CENSP 141
Db 62 AF--DGSBMSKEEDSIWFRPITLLODSGLYACVAINRSTYCMKVSIISLTGVEDDTGLCTNSK 119
0Y 142 MKLPHKUYIEG----IQRTCPNVDSYFPSSVKPRTTYMGCYKIQNFNNVPEGBML 197
Db 120 MK-----YFEKALISKEKESICRDIEDFLPTEPEELMWKECKRTKTRWSYIFKQDTL 173
198 SFLLALISNNGUYTCVVYTPYNGCRFTHLTRITLYKVVSGPKNAVAPVHSBNPH--VWYE 255
174 LIREVBEDDIGNYTELKY--GGFVVRRTTELVT--APLTDKPKLYLWMEKTLTIOE 228
0Y 256 KERGEELLIPCVYSPFLMDSRNEBWTMTIDOKKDDI-----ITDYINESISHKTED 309
Db 229 TOLGSANULTCAAFEGYSGDVSPLLYMMKGEKFIEDIDENRWESDRI--LKEHGEQ 285
0Y 310 ETRTDLISKUTSBDLRSYVCHARSAKGEVAKAAKYOKUPAPRYVELACFGATVL 365
Db 286 EVSISLI--VDSYEBEDL--GNVSCYVENONGR--RHASVLIHKREMLTYVELAGLGLAILL 341
0Y 370 LVVILIIVYVHYTMLEMLFTRAHFGTDETILIDKKEYDIIYVSYAR-----NAEEEP 422
Db 342 LNVCLVTIYKCYKIEIMFYRNHFPAEELDDGNMDYDYLISYTYVDPDQNMQETGEEREF 401
421 VLLTGRVLNENFGYKLCIFRDSLPQGNTEVAEAFDIORSRMIWVLPDPYTESKISM 480
Db 402 ALEILPDMLEKHGYKLFIPRBDLIPCTYIIBDVARCYDQSKRIIIVMTPIYVVRBQMSI 461
0Y 481 LEFKGVMCONSIAF--KLIVETRPLEHHPGLDLKE-----SYFVYSMTGEX 528
Db 462 --FELETRIRNMLVNGELIKVILIECSELR-----GIMNVOEVALKMTIKLTLYKMGPK 515

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QY 529 SKHSKFWALRALPLR-----SLSSSGNNECSSQSDISLD 568
      |||||:
Db 516 CNKNSKFWRLQYEMPKKIEPTTHEQALDVSEQCPFGEQLQVSALISMAASTIALATA 575
      |||||:
QY 569 HVQRR-----RSRLKEPELOSSEPAASGPAPGMSGHRKSSATRCCTVYEGEN 621
      |||||:
Db 576 HPDLSTFTHTHTSHOMQOKYTRSYEDV--PPTGTLPLTISIGNQHTYCNIPMTLNGQR 633
      |||||:
QY 622 HLRNKSRAEIHNOFOMETHLCKEVPQES 649
      |||||:
Db 634 PQTSKREQNDPEAHNTMSALPLPLPRET 661
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RESULT 9
US-10-011-548-28
; Sequence 28, Application US/10011548
; Publication No. US20030055218A1
; GENERAL INFORMATION:
;

APPLICANT: Timans, Jacqueline C.
 Debets, Johannes Eduard Maria
 Antonius
 Sana, Theodore R.
 Bazan, J. Fernando
 Kastelein, Robert A.
 TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and
 Methods
 NUMBER OF SEQUENCES: 36

NUMBER OF SUBJECTS: 60
CORRESPONDENCE ADDRESS:
ADDRESSER: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent-In-Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,548
FILING DATE: 22-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/173,151
FILING DATE: (Unknown)
APPLICATION NUMBER: US 60/065,778
FILING DATE: 17-NOV-1997
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
APPLICATION NUMBER: US 60/078,418
FILING DATE: 18-MAR-1998
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34, 090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
REGISTRATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 541 amino acids
TYPE: amino acid
STANDARDNESS: No. US20030055218A1 Relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 28;
US-10-011-548-28

Query Match 14.4%; Score 528; DB 9; Length 541;
Best Local Similarity 30.0%; Pred. No. 3e-34;

Matches 174; Conservative 93; Mismatches 215; Indels 98; Gaps 27;

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QY 4 LMCVSLYFYGILOSDASERCDDWGLDTR-QIOVFDEPARIK-CPLEHFLKFNYSIA 61
DB 10 LMTLISV-----STAESC-----TSRPHITVEGEFPYLKHC-----SCSLA 46
QY 62 HSGAGLT-ITWTRQDDLEBPINFLPBRISKEVDLMFRPLTNDGNTYCLMNTT 120
DB 47 HEETTTKSWYKSGSGOEHE-LNPR-SSSRIALHDCVLEFWEVLELNDGTSYFFOMKNYT 104
QY 121 YGSKVAPLEVVQ--KDSCFN---SPMKLPVHKLTYEIGQRTCPVNDGYPPSSVKPT 174
DB 105 Q-----KKKLVIRRNKSCFTEKROVTSKIVEKPF-----QITCEN--SYQTLVNST 152
QY 175 ITWYMGCKYKIONFNVIPE-GMNLSPILALISNNGYTCVVTYPENGRTFHLTRTLTVKV 233
DB 153 -SLYKCKKULLENNKNPTIKNAEF-----EDGYYSCHVFLHNGKLFNITKTENITI 206
QY 234 VSGPKNAVPPVIVHSNDHVVYEKEPGBELLIPCTVYFSFLMDSRNEVWMTIDGKPPDIT 293
DB 207 VEDRSNIVPVLGPKNHVAVEL--GKNVRLNC---SALINEBDVIYMMFGEENGSDPN 260
QY 294 IDVTINESISHRTDETRT-----QILSIKVTSEDLKRSYVCHASAKGEVAKAA 345
DB 261 I-----HEEKEMRIMTPEGKMHASKVLRLENIGESNLAVLYNCTVASGTGDTKSF 311
QY 346 KVKOK-----VPAPRYVELACGFGATVLL--VVILIIVVHYVWLEMLVFPYRAHFGTDE 397
DB 312 ILVRKADMADIPGHVFT---RGMIIAVLIVAVVCLVTVYRVDLVFPHHLTRDE 367
QY 398 TILDKREYDIYVSAR-----NAEEEFVLTLRGVLENEFGYKLCIFDRDSLPGNTVE 452
DB 368 TLVDGKYDYAFVSLKECRPENGHEHTFAVEILPRVLEKHFYKLCIFERDVPVGAAYVD 427
QY 453 AVPDFIORSRMTVLSPOVTEKSIEMLEFKL-GWMCQNSIAKTLIVVERPLEHH-- 509
DB 428 EHSLEKSRRLIIVLSKSYNSNEVRYELSGHLEALVERKI--KILILEFTVDTFTFL 485
QY 510 PGILQLESVSVFWMGKESKSHSGKFKMALRLALPLRSL 549
DB 486 POSIKLIKSHRVLKMKADKSLSYNSRFWKLLYLMPAKTV 525

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RESULT 10

US-09-981-421-4
Sequence 4, Application US/09981421
Patent No. US20020098185A1

GENERAL INFORMATION:
APPLICANT: Sims, John E.
APPLICANT: Mohler, Kendall M.
APPLICANT: Born, Teresa L.
TITLE OF INVENTION: METHODS FOR TREATING IL-18 MEDIATED DISORDERS
FILE REFERENCE: 3086-A
CURRENT APPLICATION NUMBER: US/09/981,421
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: US 60/241,408
PRIOR FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 541
TYPE: PRT
ORGANISM: Homo sapiens
US-09-981-421-4

Query Match 14.4%; Score 528; DB 10; Length 541;
Best Local Similarity 30.0%; Pred. No. 3e-34;
Matches 174; Conservative 93; Mismatches 215; Indels 98; Gaps 27;

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QY 4 LMCVSLYFYGILOSDASERCDDWGLDTR-QIOVFDEPARIK-CPLEHFLKFNYSIA 61
DB 10 LMTLISV-----STAESC-----TSRPHITVEGEFPYLKHC-----SCSLA 46
QY 62 HSGAGLT-ITWTRQDDLEBPINFLPBRISKEVDLMFRPLTNDGNTYCLMNTT 120
DB 47 HEETTTKSWYKSGSGOEHE-LNPR-SSSRIALHDCVLEFWEVLELNDGTSYFFOMKNYT 104
QY 121 YGSKVAPLEVVQ--KDSCFN---SPMKLPVHKLTYEIGQRTCPVNDGYPPSSVKPT 174
DB 105 Q-----KKKLVIRRNKSCFTEKROVTSKIVEKPF-----QITCEN--SYQTLVNST 152
QY 175 ITWYMGCKYKIONFNVIPE-GMNLSPILALISNNGYTCVVTYPENGRTFHLTRTLTVKV 233
DB 153 -SLYKCKKULLENNKNPTIKNAEF-----EDGYYSCHVFLHNGKLFNITKTENITI 206
QY 234 VSGPKNAVPPVIVHSNDHVVYEKEPGBELLIPCTVYFSFLMDSRNEVWMTIDGKPPDIT 293
DB 207 VEDRSNIVPVLGPKNHVAVEL--GKNVRLNC---SALINEBDVIYMMFGEENGSDPN 260
QY 294 IDVTINESISHRTDETRT-----QILSIKVTSEDLKRSYVCHASAKGEVAKAA 345
DB 261 I-----HEEKEMRIMTPEGKMHASKVLRLENIGESNLAVLYNCTVASGTGDTKSF 311
QY 346 KVKOK-----VPAPRYVELACGFGATVLL--VVILIIVVHYVWLEMLVFPYRAHFGTDE 397
DB 312 ILVRKADMADIPGHVFT---RGMIIAVLIVAVVCLVTVYRVDLVFPHHLTRDE 367
QY 398 TILDKREYDIYVSAR-----NAEEEFVLTLRGVLENEFGYKLCIFDRDSLPGNTVE 452
DB 368 TLVDGKYDYAFVSLKECRPENGHEHTFAVEILPRVLEKHFYKLCIFERDVPVGAAYVD 427
QY 453 AVPDFIORSRMTVLSPOVTEKSIEMLEFKL-GWMCQNSIAKTLIVVERPLEHH-- 509
DB 428 EHSLEKSRRLIIVLSKSYNSNEVRYELSGHLEALVERKI--KILILEFTVDTFTFL 485
QY 510 PGILQLESVSVFWMGKESKSHSGKFKMALRLALPLRSL 549
DB 486 POSIKLIKSHRVLKMKADKSLSYNSRFWKLLYLMPAKTV 525

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RESULT 11

US-10-157-447-2
Sequence 2, Application US/10157447
Patent No. US20020143155A1

GENERAL INFORMATION:
APPLICANT: Parmet, Patricia et al.
TITLE OF INVENTION: Receptor Designated 2F1
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/157,447
FILING DATE: 28-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/576,176
FILING DATE: <Unknown>
APPLICATION NUMBER: 09/110,618
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.

REGISTRATION NUMBER: 32,172.
 REFERENCE/DOCKET NUMBER: 2619
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 233-0644
 TELEX: 756822
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 541 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-10-157-447-2

Query Match 14.4%; Score 528; DB 12; Length 541;
 Best Local Similarity 30.0%; Pred. No. 3e-34;
 Matches 174; Conservative 93; Mismatches 215; Indels 98; Gaps 27;

QY 4 LMCVSLYFYGLQSDASERCDMDGLDTR-QIOVFEDPARIK-CPLFEHLKFNSTAG 61
 DB 10 LMTLSV-----STRASC-----TSRHITVEGEFPYLKAC-----SCSLA 46
 62 HSAGLTL-IMWTRDRDLPEPINFRLPENRISKEVDLMFRPTLLNDTGNVTCMLRNTT 120
 DB 47 HEIETTSWTKSSGSGQHEVE-LNPR-SSSRILALHDVLEFMPVELNDTGSVFQMKMYT 104
 QY 121 YCSKAPLELVQ-KDSGPN-----SPMKLRYHKLRYTGYQRTCPNVDDGYFBSVYPT 174
 DB 105 Q-----KMTLANYIRRNKSCFTEKOVTSKIVEYKFP-----QITCEN--SYQTLVNST 152
 QY 175 ITWYWCYKIQNFNNVPE-GMNLFLIALISNNGNYTCVVTYPENGRTPHLTRLTYKV 233
 DB 153 -SLYKCKKLLKNNKPTIKNAEF-----EDQSYSCVHFLHNGKLFNITKTENIT 206
 QY 234 VCSFPAVPPVILSPNDVVEKEGPEELLIPCTYFSPFLMDSRNEVMTIDGKKPDIT 293
 DB 207 VEDRNIYFVLGPKLNVAVEL-GKRVRLNC-----SALNBEVITYMGEENGSDPN 260
 QY 294 IDVTINESISHRTDEFTT-----QIJSIKKVTSEDLKRSYVARSAGKEVAFAA 345
 DB 261 I-----HEKEMRLMTPGKMKHASKVLRILENIGESNLAVLNCVASTGTGDTXSF 311
 QY 346 KYKOK-----VAPRYVTELAGFGATYLL-----VILIVVHVWLEWVLFRAHFGDE 397
 DB 312 ILVRADADLFGHVF-----RGMIIAVLILVAVGLVTVCVIRVDLVTFRHLTRDE 367
 QY 398 TILDKEXYDIYVSAR-----NAEEEFVLLTLRGVLENERGYKLCIFDRDSLPGQNTVE 452
 DB 368 TLTDKTDAPFVSLKEGRPENGEHTFAVELPRVLEKHGYKLCIFERDVPAGAVVD 427
 453 AVFDIQSRRNIYVLSPDYTEKISMLDFGL-GVMCONSITATLYIVETRLPLEHPI-- 509
 DB 428 EIHSLIEKSRRLIYLSYSYMSNEVRTELESGLHEALVERKI-KIILIEFPVVDFTFL 485
 QY 510 PGIIQKESVSPVSWKSGSKSGKFWKALRLALPLRSL 549
 DB 466 POSLKLKSHRVLKKADKSLSYNSRFMNLLIYMPAKTV 525

RESULT 12

US-10-011-548-32
 Sequence 32, Application US/10011548
 Publication No. US20030055218A1

GENERAL INFORMATION:

APPLICANT: Timans, Jacqueline C.
 Debetts, Johannes Eduard Maria
 Antonius
 Baza, J. Fernando
 Kastelein, Robert A.
 TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods

NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DNAX Research Institute
 STREET: 901 California Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/011,548
 FILING DATE: 22-Oct-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/173,151
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 60/065,776
 FILING DATE: 17-Nov-1997
 APPLICATION NUMBER: US 60/078,008
 FILING DATE: 12-Mar-1998
 APPLICATION NUMBER: US 60/081,883
 FILING DATE: 15-Apr-1998
 APPLICATION NUMBER: US 60/095,987
 FILING DATE: 10-Aug-1998
 APPLICATION NUMBER: US 60/078,416
 FILING DATE: 18-Mar-1998
 APPLICATION NUMBER: US 60/062,066
 FILING DATE: 15-Oct-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Ching, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DX0767X
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 852-9196
 TELEFAX: (650) 496-1200
 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 555 amino acids
 TYPE: amino acid
 STRANDEDNESS: No.
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 32:
 US-10-011-548-32

Query Match 13.5%; Score 496; DB 9; Length 555;
 Best Local Similarity 26.4%; Pred. No. 1.2e-31;
 Matches 155; Conservative 109; Mismatches 230; Indels 94; Gaps 26;

QY 6 CVALSYFYGLQSDASERCDMDGLDTRKQIOVFEDPARIKCPLFEHLKFNSTAGSAG 65
 DB 26 CVICNVF-----VLGGEPLAISCPLV-----ITLPLMHS-D 54
 QY 66 LTLWTRDRDLPEPINFRLPENRISKEVDLMFRPTLLNDTGNVTCMLRNTTYSKV 125
 DB 55 YNLTWY--RNGSNM--PITTE-RRARIHQKGLMFTPALLEDGLYECVEFRSINRSKQ 109
 QY 126 APFLVQKOS--CFNSPMKLPVHKLTYEGIORITCPNVGY-FPSVSKPTITWYMGCY 182
 DB 110 IINLKVNDGCLFNGEMK--YDOIYKSNAGKILCPDLNFPDEBNINPEIHMYECK 167
 QY 183 K-IQNFNNVIRPGM-LSPFLIALISNNGNYTCVVTYPENGRTPHLTRLTVKVGSPKN 239
 DB 168 SGFLEDKRLVLABGEMAILILNVTIODKGNVTCMVVITYMGKOVNVSRTNMLRYVESPLK 227
 QY 240 AVPVYHSPNDHVVEKEGPEELLIPCTV--YSEFLMDSRNEVMTIDGKKPDITIDV 296
 DB 228 MRPEFTY-PNNNTI-EVELGSHVMECNVSSGVYGLL-----PYWQVNDDEDVD--SFDS 277

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/731,175
FILING DATE: 05-Dec-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/924,777
* FILING DATE: 2000-01-31
APPLICATION NUMBER: US 07/963,928
FILING DATE: 20-OCT-1992
APPLICATION NUMBER: US 08/027,750
FILING DATE: 08-MAR-1993
APPLICATION NUMBER: US 08/183,563
FILING DATE: 18-JAN-1994
APPLICATION NUMBER: US 08/381,603
FILING DATE: 27-JAN-1995
APPLICATION NUMBER: US 08/567,710
FILING DATE: 05-DEC-1995
APPLICATION NUMBER: US 08/685,212
FILING DATE: 23-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 018484-002280US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 576 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-731-175-4

Query Match 13.2%; Score 484.5; DB 10; Length 576;
Best Local Similarity 25.8%; Pred. No. 1,1e-30;
Matches 153; Conservative 120; Mismatches 225; Indels 95; Gaps 27;

QY 34 QIYFPEBPARI-----KCPFEHFLKFNSTANASAGITLIWYTRDRIEE 81
DB 21 EIDVCTEYPNOIVFLSVNEIDIRKCPILTPNKM-----GDTIIMY-----KNSKT 67
QY 82 PINRLEPNRISKEKDVLMFRPTLLNDNGYTCMLRNTTYSKVAFLVVOXDS--CFN 139
68 PISAD-RDSRHQONHEHLMFPAKVEDSGYYCYVRSNTYCLTKRYVTVALENDGLCY 126
QY 140 SPMKLPVHKLYIEVGIORITCPNVGYE--PSSVKTITTYMGCTYKIONFNNVIREGNL 197
DB 127 TOAFEP--QRLHIA-GDGLVCPYV--SYKDNENELPEVOWKNC-KPELLNVSPFGKD 182
QY 198 SFLLALIS--NNGVYTCVYTPENGRTFLRLTLTKVAVGSPKAVPVYHSPNDAYVE 255
DB 183 KLVARNVAEERGDYICMSYTFRGKQPVYRVIOPIITIDENKRD-RVVIISPRNETI-E 240
QY 256 KEPEEBLIPCTVVFSPFLMDSRNEVWMTIDGKKPDITIDVTINES-----ISHRT 307
DB 241 ADRESMTOLICNTVGOF-----SDLVYWKNGS-----ELEMNDPLAEDYQFHEHST 289
QY 308 EDE-TRTOILSIKVTSEDLRSYVCHARSAKGEVAKAKYKQVAPRYVELACGFGA 366
DB 290 KRKYTLITLTLNISSEKVSQFYRVPFCVAKNT--NIFESAHVOLIVPVDPKVILGFTI 347
QY 367 TVLLVVLIVVHYVWMLTFYRAHFG--IDETILDKKEYDIYVSARNAE-----E 418
DB 348 LTAIVTCVCVCIYKVFKVDIVLYMYRDSGGLPSKASDKTKTDAYILYKTLGEGSFSOLD 407
QY 419 EFVLLTTLRGVLENEFGYKLCIFDRSLPLGNTVEAVDFIQRSRRIIVLSPD----- 471

DB 408 TTFEKLPLEVLGCGFYKLFYGRDDYVGEDTIEVNNVKSRRLLIILVRMGFSWL 467
QY 472 -YTESISLMEKLGVMCONSIATLIVERRPL--HPHPIIQ-LNESVFSVMKG- 526
DB 468 GGSSEQIAL---YNALIQEGI--KIVILLEKEIDYERMPDSIOFIKQKGVICWSD 521
QY 527 --EKSHSGSKFWKALRLALPLRLSASSGWNESCSSQSDISDHVORRRRL 577
DB 522 FQRPQSAKTRFWKALRYQMPAQRSS-----PLSKRLITLDPVADYKEL 567

RESULT 15
US-10-011-548-29
Sequence 29, Application US/10011548
Publication No. US20030055218A1
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
Debets, Johannes Eduard Maria
Antonius
Sana, Theodore R.
Bazan, J. Fernando
Kaetelein, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,548
FILING DATE: 22-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/173,151
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-9196
TELEFAX: (650) 496-1200
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 537 amino acids
TYPE: amino acid
STRANDEDNESS: NO. US20030055218A1 Relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-011-548-29

Query Match 13.1%; Score 479; DB 9; Length 537;
Best Local Similarity 27.4%; Pred. No. 2,7e-30;
Matches 167; Conservative 102; Mismatches 218; Indels 122; Gaps 30;

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QY      1 MTLIMCVSLYFYGILQSDASERCDDWGLDTRQIQVFEDEPARIK-----CPLFEHFLK 55
      6 LILTLCT-----LIVKSAKSCIH-----RSQIHVEGEPFYLKPGGISAPVHRN--- 50
QY      56 FNVSTASAGITLWYWTRODRDLLEPINFRLPENRISKEQVLMFRPTLNDNGNTCM 115
      51 ---ETA-----TWKMFQGSASHEVRELNNRSP--RVTFHDHLEFMPVEMEDEGTYISQ 100
QY      116 LRRTTYSKVAFPLEVVQ--KDSGFNSPMKLPVHKLYIEYGIQ-----RITC--PNVDGY 166
      101 VGN-----DRNMWTLNVTKRKHGSCFSD-----KLVTSRDVEYKSLHITCKNPNTBEL 149
      167 PSSSVKPTITM-YMGCYKIQNFNNVIEGQNLSEFLIALISNNGNYTCVVTYPENGRTFHL 225
      150 IQD-----TWLYNCKEISTKPRILND-----AEFGDEGYSCVFSVHNHNGTRYNI 195
QY      226 TRRLTVVGSPPKRAVPVPIHSPNDHYVEKEPGEELLIPCTVYFSLMDSRNEVMTID 285
      196 TKTVNITVI-EGRSKVPALGPCKECV-GVELGQDVELNC---SASLNKDLFTWSI- 248
QY      286 GKRPDDITIDVTINESISHRTEDET-----RTQILSIKVTSEDLKRSYVCHARSA 337
      249 -RKED-----SSDPNVQERKETTWTWISGKLAASKILRQKITENYLVNLVINGTVANE 301
QY      338 KGEVAKAKAYKQK---VPAARYVELACGFGATVLT-----VVLIVYHVWVLEM 385
      302 EADITKSFVLVRKEIPDIPGHVFT-----GGTVVLVASAANVCIVILCVYKV---DL 352
QY      386 VLFYRAHFGDETLIDGKETDIYVSAR---NAEEBEFVLLTLRGVLENEGFKLCIF 440
      353 VLFYRRIARDEDTLTDGKTYDAFVSYLKECHPENKEEYTFVAVETLPRVLEKQFGYKLCIF 412
QY      441 DRDSLPGGNTVEAFDFIORSRMIVLSPDYTEKISIMLEFRL-GVMCONSIAATKLIV 499
      413 ERDVVPGGAVVEEIHSLIEKSRRLITVLSOSYLTNGARRBLESGLHEALVERKI--KILL 470
QY      500 VEYRPLEPH--PGILQKESVSFVSWKGEKSKHSGSKFMKALRLALPLRSLASSGMNE 557
      471 IEFTPANITFLPPSLTLKSYRLKWRAD-SPSMNSRFWMKNUVYLMPAKAVKP---WRE 526
      558 SCSQSQSDIS 566
      527 ESEARSVLIS 535
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Search completed: April 23, 2003, 09:00:26
Job time : 48 secs

Db 421 VLLTLRGVLENEFGYKLCIPDRDSLPGIVTDETLFIQSRRLVVLSPVYVLTQAL 480
 QY 481 LEFLKGVMCNSIATK---LIVERPLEPHEPGLQKES---VSFVSKGSKXRG 533
 Db 481 LELKAGL---ENMASRGNINVLVQKAVKDMK---VKELAKRAKTLVTKWKGSKXKPPQ 535
 QY 534 SKFWALRLALPLRSLSASGNNES 558
 Db 536 GRFWKQLQVAMPVK---SPRWSSN 557

RESULT 2
 J01526
 interleukin-1 receptor I precursor - chicken
 C/Species: Gallus gallus (chicken)
 C/Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 29-Sep-1999
 C/Accession: J01526
 R/Guida, S.; Heguy, A.; Melli, M.
 Gene 111, 239-243, 1992
 A/Title: The chicken IL-1 receptor: differential evolution of the cytoplasmic and extra
 A/Reference number: J01526; MUID:92175529; PMID:1531799
 A/Accession: J01526
 Molecule type: mRNA
 Residues: 1-555 <GUI>
 A/Cross-references: GB:M81846; NID:g212206; PIDN:AAA48924.1; PID:g212207
 A/Experimental source: embryo
 C/Superfamily: interleukin-1 receptor type I
 C/Keywords: cytokine receptor; transmembrane protein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-555/Product: interleukin-1 receptor I #status predicted <INT>
 F:339-359/Domain: transmembrane #status predicted <TRA>

Query Match 13.5%; Score 496; DB 2; Length 555;
 Best local similarity 26.4%; Pred. No. 1.7e-29;
 Matches 155; Conservative 109; Mismatches 230; Indels 94; Gaps 26;

Db 6 CVVSLYFGIIGDSERCDWGLDTMRQIQVFEDEPARICPLEHFLKKNYSTAHSG 65
 Db 26 CVTCNP-----VLGEPRALISCPV-----ITLPMHS-D 54

QY 66 LTLVYWRQDRLEEPINFLPERNISKEKQVLFWRPTLLDNTGNTCMLENTYCSKV 125
 Db 55 YNLTVY--RNGSNM--PITTE--RRARIHQKGLWFIPLALEDGLVCEVRSNRSKQ 109

QY 126 APPELVOKDS--CFNSPKLPHKLYIEYGIQITCPNVQY--PPSVKPTTYWGCY 182
 Db 110 IINLVKFNKDNGLCFNGEKK--YDOIIVSANAAGKIICPLENFKQEDNINDEIHWYKECK 167

QY 133 K--IQNFNNVIREGN--LSFLALISNNGNTCVVTPENGRTFLHRTTLTVKVGSPKN 239
 Db 168 SGFLDKRLVLAEGENALILNVTTIODKGNVTCRVVYTYMGQVNSHTMLEVESPLK 227

QY 240 AVPPYIHSFNDHVVYEKEPEELIPCTV---YFSLNDSRNEVMTIDGKKPDDITDV 296
 Db 228 MRPEPIY--PNNTI--EVELGSHVMECAVSSGVGL-----PYQVNDDEVD--SFDS 277

QY 297 T-----INESISHTDEDTQTQIISIKKVTSEDLKRSYVCHASAKAEVAKAVKOV 351
 Db 278 TYREOFYEEMPHGIAVSGTK---FNISEVKLKDYAVKFCFIYDSOEFSTYILEH-- 332

QY 332 PAPRTVELAGFGATVLLVLLVYVHYVLMELVFRYA--HFGTDTIIDGKEYDYV 409
 Db 333 PVQNIIRGYLIGGISLILFLPLILVYKIFKIDIVLMYRSSCHPLGKKSVDGKIYDNYV 392

QY 410 SYARAAE-----EEEFVLLTLRGVLENEFGYKLCIFDSDLSFGNTVAEVPDIQSRM 464
 Db 393 LYPKRESGLVSSDIPALKILPEVLERQGVNLFIFGRNDLAGAIVDVTDEKIHQSRV 452

QY 465 IYVLSP-----DYVEKSIISMLEFLKGVMCNSIATKLIVETPLP---HPHEIL 513
 Db 453 IILVPEPSCYGILEPDASERKHLAV---YNALIDGI--KILILEKTEIDYANNPESIK 506

QY 514 QKESVYFVSMKG---EKSHSGSKFWKALRLALPLRSLSASGNNES 558

Db 507 YVQKYGALIRMTGDFSESHSASTRFKVKRYHYHMPKRGSSSGFHLIS 554
 Db 156526

RESULT 3
 interleukin 1 receptor type I - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 29-Sep-1999
 C/Accession: I56526
 R/Hart, R.P.; Liu, C.; Shadiack, A.M.; McCormack, R.J.; Jonakait, G.M.
 J. Neuroimmunol. 44, 49-56, 1993
 A/Title: An mRNA homologous to interleukin-1 receptor type I is expressed in cultured
 A/Reference number: I56526; MUID:9326794; PMID:7684399
 A/Accession: I56526
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-590 <RES>
 A/Cross-references: GB:M95578; NID:g451305; PIDN:AAA16196.1; PID:g451306
 C/Superfamily: interleukin-1 receptor type I
 C/Keywords: cytokine receptor

Query Match 13.5%; Score 493.5; DB 2; Length 590;
 Best local similarity 26.5%; Pred. No. 2.9e-29;
 Matches 153; Conservative 105; Mismatches 230; Indels 89; Gaps 25;

QY 47 CPLEFHLKRYSTAHNAGLTLVYWRQDRLEEPINFLPERNISKEKQVLFWRPTLL 106
 Db 60 CPLPNEH-----GGTIIWY---KNDSKTPISAD--KDSRIHQNHLMFVPAKM 105

QY 107 NDTGNTCMLENTYCSKVAPPELVOKDS--CFNSPKLPHKLYIEYGIQITCPNVQ 164
 Db 106 EDSGYTCIMNSSTYCLKTKITMSVLENDPGLCTNTQASF--IQRLHYA--GGSIVCPYLD 163

QY 165 GYF--PSSVKPTTYWGCYKIQNFNNVIREGN--LSFLALISNNGNTCVVTPENG 216
 Db 164 -FFDEENNELPKVQYVNGCKLP-----LDDGNFFGFKNKLMNVAEHRGNTCRTSY 217

QY 217 PENGRTFLHRTTLTVKVGSPKNAVPPYIHSFNDHVVYEKEPEELIPCTVYFSLNDS 276
 Db 218 TYQCKQVPRVIRVIFITIDSKRD--RPVIMSPREIM--EADPGSTIOLICVNTGQF--- 271

QY 277 RNEVMTIDGKKP--DITIDVTINESISH--SRTEDETRQTQIISIKKVTSEDLKRSYVCHA 334
 Db 272 TDVLVYKMGSEIWDPEILAEDYQFLHPSAKKTLITTLANSYKVSQYRRPFCFV 331

QY 335 RSAGGVAKAKVQKVPAPRYVELACFGATVLLVLLVYVHYVLMELVFRYAHFG 394
 Db 332 KNT--HILETAHVLLVVPDPKQVLLGFGALPATAVFCACIYKVPKVDIVLWYRDCS 389

QY 395 --TDETLIDGKEYDYIYSYARAAE-----EEFVLLTLRGVLENEFGYKLCIFDRSLP 446
 Db 390 DFLPRKASDGTIYAVLYPPTYGEGSPAYLDTVFLLPLPEVLGQFGYKLPICGRDYV 449

QY 447 GGNTEAVFDIORSRMIVVLSPPDYTEKSIISMLEFK--LGVMCNSIA-----TK 496
 Db 450 GEDTIEVTENVAKSRKILILVVD-----MGSRCLOSSSEBOQIAYDALIREIK 501

QY 497 LIVERPLEPHEPGLQKESVSFV-----WKG---EKSHSGSKFWKALRLALPL 546
 Db 502 IILPELEKIQVY---KMPEIQFIKQKHCALCMSGDFKRPQSAKTRFWKNIRYQMDA 557

QY 547 RSLASASGNNESGSGDISDHYQRRSRKAKEPEL 583
 Db 558 QRRS-----PLSKHMLTLDPVLTDTKEKLOAETHL 587

RESULT 4
 A32604
 interleukin-1 receptor precursor - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 29-Sep-1999
 C/Accession: A32604

R.Sims, J.E.; March, C.J.; Cosman, D.; Widmer, M.B.; MacDonald, H.R.; McManan, C.J.; Gru S.K.
 Science 241, 585-589, 1988
 A:Title: cDNA expression cloning of the IL-1 receptor, a member of the immunoglobulin su
 A:Reference number: A32604; MUID:88290679; PMID:2965618
 A:Accession: A32604
 A:Molecule type: mRNA
 A:Residues: 1-576 <SIM>
 A:Cross-references: GB:M20658; GB:M29752; NID:918300; PIDN:AAA39279.1; PID:9309399
 C:Superfamily: Interleukin-1 receptor type I
 C:Keywords: cytokine receptor; glycoprotein; phosphoprotein; transmembrane protein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-576/Product: interleukin-1 receptor #status predicted <INT>
 F:339-359/Domain: transmembrane #status predicted <TM>
 F:46-199,145-199,251-315/Disulfide bonds: #status predicted
 F:63,103,174,236,252,266,300/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 13.2%; Score 484.5; DB 2; Length 576;
 % Local Similarity 25.8%; Pred. No. 1.4e-28;
 Matches 153; Conservative 120; Mismatches 225; Indels 95; Gaps 27;

QY 34 QVQVEDDEPARI-----KCPLEHFLKFNYSRAHAGLLIYVWTRQDDLEE 81
 DB 21 EIDVCTEYENQIVLFLSVEIDIRKCPLEPNKMH-----GDTIIYV---KNDSKT 67
 QY 82 PINFLPERISKEKDVLFRRPTLNDTGNNTYTCMLNTYCSKVAPELVEQKDS--CFN 139
 DB 68 PISAD-RDSRIHQNHMLFVPAKVEDSGYYCIYVNSTYCLTKTYVTVLENDPLGLTS 126
 QY 140 SPMKLPVHKLYIEYGIQRTICPNVDYF--PSSVKPTITWYMGCYKIQNFNNVPRGMIL 197
 DB 127 TQATFP-QELHIA-GDGSIVCFYV-SYFKDENNELPEVQMYKNC-KPLLDNVSPFGVND 182
 QY 198 SFLIALIS--NNGNTCVVTPENKRTFHLTRLYKAVGSPKNAVPRPIHSHNDVVE 255
 DB 183 KLVNRVNAEHHGDYICRMSYTFRGKQYPTRYIOPITIDENKRD-RPVLSPRNETI-E 240
 QY 256 KEGREELLPCTYVFSFLMDSRNEVMTIDGKKRPDITIDVTINES-----ISHSRT 307
 DB 241 ADPGSMIQLICVNTGQF---SDLVYWKMGNS-----EIEENDPLAEDYFVHHPT 289
 QY 308 EDE-TFTQIISIKRTVSEDLKSYVCHASAKGEVAAKVKQVPAPIRYVELACGFGA 366
 DB 290 KKKYTLITLNTISEVKSQFRYPFCIVKNT--NIPESAHVQIYVDPKQVYLIGCFII 347
 QY 367 TVLLAVITLVHRYVLEWLFYRAHFG--TDETIIDGKRYDIYVSARNAE-----E 418
 DB 348 LVATIVCCVCYKVFVNDIVLWTRDSCGFLPSKASDGKTYDAVYIIPKTLGSGFSDDL 407
 QY 419 BPTLLTRGVLENERGYKCIPIRDSLPGNTVEAVPFIORSRMIVLSPD-----471
 DB 408 TTPFKLLEPELESGQFGYKLPFYGRDYYGEDTIEVTNENKSKRLITILVRDMGFSWL 467
 QY 472 -VYTESISMLEEKLGVMCNCSITATKLIIVERAPLE--HPHGILO-LKESVSFVSMKG- 526
 DB 468 GGSSEEQIMAI-----VVALQDEGI--KIVLLELEKIDYEMKPSISQPIQKHGVICMSGD 521
 QY 527 --EKSHSGSKFKALRLALPLRLSASSGKNSSCSQSDISIDHYQRRSRL 577
 DB 522 FDERPQSAKTRFKNRLRYQMFAQRSS-----PLSKHRLITLDPVADTEKL 567

RESULT 5
 S29498
 lymphocyte antigen ly84 precursor - mouse
 N:Alternate names: 38.5K T1 glycoprotein; ST2L protein
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #ext_change 01-Dec-2000
 C:Accession: S29498; A33541; S17657; S07054
 R:Yanagisawa, K.; Takagi, T.; Tsukamoto, T.; Tetsuka, T.; Tomioka, S.
 FEBS Lett. 318, 83-87, 1993
 A:Title: Presence of a novel primary response gene ST2L, encoding a product highly simi
 A:Reference number: S29498; MUID:93170492; PMID:7916701

A:Accession: S29498
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-567 <YAN>
 A:Cross-references: EMBL:D13695; NID:9286100; PIDN:BAA02854.1; PID:9286101
 R:Klemmer, R.; Hoffmann, S.; Werenkold, A.K.
 Proc. Natl. Acad. Sci. U.S.A. 86, 5708-5712, 1989
 A:Title: Serum- and oncoprotein-mediated induction of a gene with sequence similar
 A:Reference number: A33541; MUID:89345536; PMID:2527364
 A:Accession: A33541
 A:Molecule type: mRNA
 A:Residues: 1-191, 'V', 193-328, 'SKECPSHIA', <KLE>
 A:Cross-references: GB:M24843; NID:9201103; PIDN:AAA40160.1; PID:9201104
 R:Tomioka, S.I.; Jenkins, N.A.; Gilbert, D.J.; Copeland, N.G.; Tetsuka, T.
 Biochem. Biophys. Acta 1090, 1-8, 1991
 A:Title: Molecular cloning of the murine ST2 gene. Characterization and chromosomal
 A:Reference number: S17657; MUID:91355215; PMID:1832015
 A:Accession: S17657
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-191, 'V', 193-328, 'SKECPSHIA', <TOM>
 A:Cross-references: EMBL:X60184; NID:954200; PIDN:CAA42742.1; PID:954201
 R:Tomioka, S.I.
 FEBS Lett. 258, 301-304, 1989
 A:Title: A putative protein of a growth specific cDNA from BALB/c-3T3 cells is high
 A:Reference number: S07054; MUID:90092495; PMID:2532153
 A:Accession: S07054
 A:Molecule type: mRNA
 A:Residues: 1-328, 'SKECPSHIA', <TO2>
 A:Cross-references: EMBL:I07519; NID:955517; PIDN:CAA6812.1; PID:955518
 A:Note: It is uncertain whether Met-1, Met-7 or Met-19 is the initiator
 A:Genetics:
 A:Gene: ST2
 A:Map position: 1
 A:Functions: 27/1, 97/2, 155/3, 210/1, 233/1, 280/2
 C:Superfamily: Interleukin-1 receptor type I
 C:Keywords: glycoprotein
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:27-337/Product: ST2 protein #status predicted <MT>
 F:60,101,107,146,176,194,225,259,278/Binding site: carbohydrate (Asn) (covalent) #st

Query Match 13.0%; Score 478; DB 2; Length 567;
 % Local Similarity 25.9%; Pred. No. 4.1e-28;
 Matches 163; Conservative 105; Mismatches 227; Indels 134; Gaps 28;

QY 4 LW--CVSLYFGLIOSDSERCDWGLDTRMQIOVFEDPARIKCPLEHFLKFNYSRA 61
 DB 9 LVALALITLPMY-LTVTESK--SSWGL-----ENBALIVRCP-----QKGRST- 49
 QY 62 HSAGITLTIWMTRODRDLKEPINFRLPERISKEKDVLFRRPTLNDTGNNTYTCMLNTTY 121
 DB 50 ----YVEVYYS---DTMESIPTQ-KRRRIYPSRRLKFLPARVDSGIYACVIRSPUL 100
 QY 122 CSKVAPELVEVQKDSCFNSPMKLPVHKLYIEYGIOR-----ITCPNVDGIFPSSVKFT 174
 DB 101 NKTGYLVNTIHKKRPSCNIPD-----YIMYSTVAGSDKNFETICTPTIDLY---NMTAP 150
 QY 175 ITYVNGCYKIQN-----FNNVIPKGMNLSTLIALISNNGNTYTCVYTPENKGRF 223
 DB 151 VQWFKRCKALOEBRFRPHRSYLFETIDVTHD-----DEGDTYCOPTHAENGTVY 198
 QY 224 HLFRLLTVKVGSPKNAVPPVHSPNDHYVEKEPEBELIIPCTVYFS----FLMDSRNE 279
 DB 199 IYVATRSFVVEEKGFSPFVITNPINNHM-EVEIGKPSIACSACFGGSHFLAD-----253
 QY 280 VVMTIDGKKRPDITIDVTINESISHSTDE-----TRTOIISIKKVTSEDLK 327
 DB 254 VLM-----QINKTVVGNGBEARIQEBEGRSSSNDMDCLTSVLRIGVTEKDS 303
 QY 328 RSYVCHASAKGEVAAKVKQVPAPIRYV-ELAGFGATVILVYVHRYVLEWLFYRAHFG 386
 DB 304 LEYDCIALMLHGMIRHTIRRRKQPIDHSIYYIVAGCSLLMFINVLVILKVFWEIVA 363

QY 387 LFRARHGTETILLDGEKDYIVSYAR-----NAEERFVLLTLRGVLENEGYKLC 438
 DB 364 LFRMDIVTPKTRNDGKLDYIYIPVYRGSAGTSHVEYFHHHTLPDVLENKCGHLYLC 423
 QY 439 IFRDRLPGNTVEAVEFDIORSRMIVLSP-----DYVTEKSIISMLFEKLGVMCONS 492
 DB 424 IYGRDILLPGDDAATVVESSISONSRRQVFLAFHMMHSKEFAVEDEIL-----HSLILQNN 479
 QY 493 IATKLYVEYRPL-EHHPGGLILKESVSF-----VSWKGE--KSKHS-GSKFPMALR 541
 DB 480 --SKVILIEHEPPLGEARLQVGDLODSLQHLVKIIGITIKMRBDHVADKQSISSKFMKVR 537
 QY 542 IALPL-RSLSSAGMNSCCSOSDISLDH 569
 DB 538 YQMFPERASKTASVAAPLSGACLDLKH 566
 RESULT 6
 G02426
 interleukin-1 receptor-related protein - human
 C:Species: Homo sapiens (man)
 C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 29-Sep-1999
 Accession: G02426
 Jovenberg, T.W.; Crowe, P.D.; Liu, C.; Chalmers, D.T.; Liu, X.
 submitted to the EMBL Data Library, February 1996
 A:Reference number: H01239
 A:Accession: G02426
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-562 <IOV>
 A:Cross-references: EMBL:U09065; NID:g1236078; PIDN:AA53237.1; PID:g1236079
 C:Superfamily: Interleukin-1 receptor type 1
 Query Match 12.1%; Score 444.5; DB 2; Length 562;
 Best Local Similarity 25.5%; Pred. No. 1,4e-25;
 Matches 148; Conservative 119; Mismatches 236; Indels 77; Gaps 26;
 QY 2 TLKCVSLVYFGILQSDASRCDDKGLTRQIQVFEDEPARIKPLFEHLEKNSTA 61
 DB 3 SLLCGISI--ALPLSTVADGCKD--IFMKNEILSASQPFAPNC-----TFPPI 47
 QY 62 HSAGLTILWTRQDRDLDEEPIFNRLPENRISKEKDVMPRPPTLLNDGNTOMLRNTTY 121
 DB 48 TSGEVSATWY---KNSKIPVS-KIIOSRIHODETWILFLPMKWDGSGVYQCYIKGRDS 102
 QY 122 CSKVAFLPEVQKDSCFNSPMKLP---VHLKYLEYG-IORITCPNVGYEPSS-VKPTI 175
 DB 103 CHRILHVLTYFEKIMCDPSIGLPLNLSDEYKQIHLGKDSLTC--HLHFPKSCVIGPI 159
 QY 176 TWYMGCKYIQNFNNVIEGKMLSFILALIS--NNGNYTCVVTYPENGRTHLTRLTVKVS 233
 DB 160 KMYDNCNEIKERPTV--LETLLVSNVSAEDRGVACQAILTHSGQYELNGLIYTSI 216
 QY 234 V--GSPKNAVPEVHSPNDHVVEKEPGEELLIPCTVYFSLMDRNEVMTITDCKKPD 291
 DB 217 TERAGYGGSPKIIY-PKNSHI-EVQGLTTLIVDCNV--TPTKDTNLRCRRVNTLVDD 272
 QY 292 ITLD-VTINESI-SH-SRTDETRTQILSIKVTSEDLKRSYVCHASAKGEVAKAKVK 348
 DB 273 YYDESKIRIEGVETHVSFRHNLVTYNTIFLEVKMEDYGLPFMCAG-----VSTAVYII 326
 QY 349 QKVAPRYTVELACGFATVLLVILVYHVMLEMTLFRANHGTDETILLDGEKDYIY 408
 DB 327 LQLPAPDPRAVLLIGLALVAVAASVATYINIFKIDIVLRSASHSTETTVGDLXAY 386
 QY 409 VSYARNAEER-----EEFVLLTLRGVLENEGYKLCIFRDSLPGGNTVEAVFDFIORS 462
 DB 387 VLYCKPKHESGRHVAVDALVNLPEVLERQCGYKLFIRGRBEPQOAVANYIDENVKCR 446
 QY 463 RMIVLVSPD-----VTEKSIISMLEFKLGVMCONSIAATKLIVVEYRPLEH----DHP 510
 DB 447 RLIVIVVESIGFGLIKMLSEEOIADV--YSALIQDGM--KVLILEKTEIDYTVME- 499

QY 511 GILQKESVSFVSMKG---EKSXHSKSKFWKALRLALPLR 547
 DB 500 SIQYIKKHGALRWHGDPFTQSOCKMTKFMKIVRYHMPRR 539
 RESULT 7
 A36187
 interleukin-1 receptor type 1 precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 29-Sep-1999
 C:Accession: A36187; S06928
 R:Stms, J.E.; Acres, R.B.; Grublin, C.E.; McMahon, C.J.; Wignall, J.M.; March, C.J.; D
 Proc. Natl. Acad. Sci. U.S.A. 86, 8946-8950, 1989
 A:Title: Cloning the interleukin 1 receptor from human T cells.
 A:Reference number: A36187; MUID:90046906; PMID:2530587
 A:Accession: A36187
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-569 <SIM>
 A:Cross-references: GB:M20658
 R:Chua, A.O.; Gubler, U.
 Nucleic Acids Res. 17, 10114, 1989
 A:Title: Sequence of the cDNA for the human fibroblast type interleukin-1 receptor.
 A:Reference number: S06928; MUID:90098789; PMID:2532321
 A:Accession: S06928
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-569 <CHU>
 A:Cross-references: EMBL:X16896; NID:g33800; PIDN:CA34773.1; PID:g33801
 C:Genetics:
 A:Gene: GDB:111R1; 111R2; D261473; 111R
 A:Cross-references: GDB:125254; OMIM:147810
 A:Map position: 2q12-2q12
 C:Superfamily: Interleukin-1 receptor type 1
 C:Keywords: cytokine receptor; transmembrane protein
 Query Match 11.6%; Score 424.5; DB 2; Length 569;
 Best Local Similarity 24.3%; Pred. No. 4,6e-24;
 Matches 129; Conservative 117; Mismatches 205; Indels 79; Gaps 24;
 QY 67 TLWYTRQDRDLDEEPIFNRLPENRISKEKDVMPRPPTLLNDGNTOMLRNTTYCSKVA 126
 DB 54 TITWY-----KDSKTPSTE-QASRIHQHCKLMFPAKEDBSGHYCVVRNSYCLRIK 108
 QY 127 FPLEVQKDS--CFNS---PMKLPVHKLVEYGIQRTCPNVGYF--PSSVAPRTTWY 178
 DB 109 ISAKFVENEPLCYNAQAIFFOKLPV-----AGDGLVCPYME-FFKNNENELPKLOMY 161
 QY 179 MGCKYIQNFNNVIEGKMLSFILALIS--NNGNYTCVVTYPENGRTHLTRLTVKVS 236
 DB 162 KDC-KPLILNHSFGVDRILVWNAEKIRGNYTGHASTYLGKQPIITRVILEPITLES 220
 QY 237 PKNAVPEVHSPNDHVVEKEPGEELLIPCTVYFSLMDRNEVMTITDCKKDDITIDV 296
 DB 221 NKPRPIYVAPAB--TMEVDLSQIOLICNTGQ-----SDIAYMKMNSVIDE--DDP 272
 QY 297 TINESI-----SHSRTDETRTQILSIKVTSEDLKRSYVCHASANGEVAKAKVK 352
 DB 273 VLGEDYVSVENPANKRSTLITVAINISEISREFKHPFTCFANHTG--IDAAYIQLIY 330
 QY 353 APRYVELACGFATVLLVILVYHVMLEMTLFR--AHRTDDETIIDGKDYI 407
 DB 331 VTNEQKHM--IGICVTLVTVIVCSVFTYKIFKIDIVLWRDSQYDFLPKASDGKTYDA 387
 QY 408 VSYARNAEER-----EEFVLLTLRGVLENEGYKLCIFRDSLPGGNTVEAVFDFIORS 461
 DB 388 YIYLPKTVGSGSDCDIFPKVLPVLEKQCGYKLFIRGRBEPQOAVANYIDENVKKS 447
 QY 462 RMIVLVSPD-----VTEKSIISMLEFKLGVMCONSIAATKLIVVEYRPLEHHPGIL 513
 DB 448 RRLIILIVRETSGRFSWLGSSSEEOIAM--YNALVODGI--KVLILEKTEIDYVE----- 497
 QY 514 QLKESVSFVS-----WKGEKS---KHSGSKFWKALRLALPLRSLSASS 553

Db 498 KMBESIKFIKQKGAIRMSGDFTQGPQSAKTRFMKVRHYHMPVGRSPSS 547

RESULT 8

333473 interleukin-1 receptor type 2 - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999

C:Accession: S33473

R.Brictul, J.; Gatti, S.; Battfai, T.

submitted to the EMBL Data Library, May 1993

A:Description: The rat insulinoma beta-cell line RIN5F express mRNA for the type 2 interleukin-1 receptor

A:Reference number: S33473

A:Accession: S33473

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-416 <BRI>

A:Cross-references: EMBL:Z22812; NID:G311407; PIDN:CAA80465.1; PID:G311408

C:Keywords: cytokine receptor

Query Match 8.2%; Score 302; DB 2; Length 416;

Best Local Similarity 25.3%; Pred. No. 5, 6e-15;

Matches 97; Conservative 67; Mismatches 153; Indels 66; Gaps 18;

```

Qy 25 DDM--GLDTRQIOVEDEPARIKCPLEHFLKFNSTASHAGLTITWYTRQDRDLEEP 82
Db 41 DCMFRGRDFKSELRL--EGEPVVALKCPVPH-----SDTSSSRSLT-TWKSQDSQCLIP 92
Qy 83 INFRLENRISKEKDVLMFRPTLLNDTGNNTYCMLENTTYSKVAFLPEVQKDSCFNSPM 142
Db 93 GD-----EPHVMVADITLWVPAVQDSGTICTFRNASHCEQMSLELKVK-----NTEA 143
Qy 143 KLPVHKLTYIEYGIQRT---CPNVDGYFPSSVKKPTITWYMGCKYKQNFNNVIEPQNLIS 188
Db 144 SPFLVS-VIOLISALSTGTLVCPDLKEFISRTDGKIQWKY-----SILLDKNKK 194
Qy 199 FLIA-----LISNN-----GNTCVATYVPENGRTFHLTTLTKVGVSPKNAVPIYHS 247
Db 195 FLSAGPTRLISNTSMGAGYRCVMTFTYBEGKEVITNIEIRVAGITTEPI-EVITIS 253
Qy 248 PNDHVVYKEPGEELLPCTVYFSPFLMDSRNEVWMTIDGKKPDITIDVT-----INESI 302
Db 254 PLFTI--PASLSRLIVPCVFLGTGTSSNTIYWM-----MANSTPISVAVPRGRVTEGL 306
Qy 303 SHSRTE-DETRIOI-LSIKKVTSEDLKRSYVCLARSAGKGVAAKVKQKVPAPRYTVEL 360
Db 307 HHQYSNDEYVAVSLIFDPTVKEDLNTDFKCVATNPRSPQSILHTYKE-----VSS 358
Qy 361 ACGFGATVLLVLLIYVYHYVL 363
Db 359 TFSWGIALAPLSLILVVGAIWI 381

```

RESULT 9

542633 Fit-1M protein - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 25-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 11-Jan-2000

C:Accession: S42633

R.Bergers, G.; Reikertorfer, A.; Braselmann, S.; Gruninger, P.; Busslinger, M.

EMBO J. 13, 1176-1188, 1994

A:Title: Alternative promoter usage of the Fos-responsive gene Fit-1 generates mRNA isoforms

A:Reference number: S42632; PMID:94178260; PMID:8131748

A:Accession: S42633

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-247 <BER>

C:Superfamily: interleukin-1 receptor type I

Query Match 7.0%; Score 256; DB 2; Length 247;

Best Local Similarity 30.8%; Pred. No. 8e-12;

Matches 70; Conservative 45; Mismatches 80; Indels 32; Gaps 9;

```

Qy 346 KVKQVPAF-RYVTELACGFGATVLLVLLIYVYHYVLEMLFYRAHFGSTDETLIDGKE 404
Db 2 RLRKQPIDHQSTYYIVAGSGLLMFNTVILTKFMLEVALFMDIMAPYKTQNDGL 61
Qy 405 YDIYVSAR-----NMBEEFVLLTLRGVLENEGYQACIFDRDLSQGNTEAVFD 456
Db 62 YDAIYIIPVFRSAGTGSVEFYHYTLPQVLENGCYGLQYGRDLFGQDAATVES 121
Qy 457 FIDSRMIVLSP-----DYTEKSISMLEPKAGMCONSTATKIVYERPL-EHPH 509
Db 122 SIONSRQVFLVLAPEHMSKEFAYEQEIAL--HSAIQNN--SKVITLMEPMGEASR 175
Qy 510 PGILOKESVSF-----VSWKGE--KSKHS-GSKFMKALRLALPL 546
Db 176 LQGLDLDSDQLVKNQGTIKMRREDHVADKQSLSSKFMKVRVYQMPV 222

```

RESULT 10

interleukin-1 receptor type II - human

C:Species: Homo sapiens (man)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999

C:Accession: S17428

R.McMahon, C.J.; Slack, J.L.; Mosley, B.; Cosman, D.; Lipton, S.D.; Brunton, L.L.; C

EMBO J. 10, 2821-2832, 1991

A:Title: A novel IL-1 receptor, cloned from B cells for mammalian expression, is expr

A:Reference number: S17428; PMID:92007725; PMID:1833184

A:Accession: S17428

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-398 <MCN>

A:Cross-references: EMBL:X59770; NID:G33796; PIDN:CAA42441.1; PID:G33797

C:Keywords: cytokine receptor; transmembrane protein

Query Match 6.9%; Score 252; DB 2; Length 398;

Best Local Similarity 23.4%; Pred. No. 3.2e-11;

Matches 79; Conservative 51; Mismatches 148; Indels 60; Gaps 13;

```

Qy 20 ASERCDDMGIDTRQIOVEDEPARIKCPLEHFLKFNSTASHAGLTITWYTRQDRDL 79
Db 24 AARSCFRGRHRYKEBRL--EGEPVALRCQVQVFWMAVSPP-----INLTWINDSARTV 78
Qy 80 --EELINFRLENRISKEKDVLMFRPTLLNDTGNNTYCMLENTTYSKVAFLPEVQKDS 137
Db 79 PGRE-----ETRMWAQCALMLPALQEDSGTYVCTTRNASYCDKMSIELRVFENTDA 131
Qy 138 FNSPMKLPHVHKYIEY-----GIQRTCPNVDGYFPSSVKKPTITWYMGCKYKQNF 188
Db 132 F-----LP-----FISYPQILITLSTSGV--LVCPDSEFTRDKTDVKIQWKSLLDKDN 180
Qy 189 NVIPBGAMTSPFI--ALISNNQNTCVVTPENGRTFHLTTLTKVGVSPKNAVPIV 245
Db 181 EKFLSVRGTHLLHVDALADAGYRCVLTFAHEGQVYITISIELRIKKKEETI-PVI 239
Qy 246 HSPNDHVVYKEPGEELLPCTVYFSPFLMDSRNEVWMTIDGKKPDITIDVTINESISHS 305
Db 240 ISPLKTI--SASISRLTIPCKVFLGTGTPPLTLMWMTAN-----DTHIESAVPG 288
Qy 306 RTEDERTIOI-----LSIKKVTSEDLKRSYVCLARSAGKGVAAKVKQKVPAPRYTV 332
Db 289 RYLEGPROEYSNNENYIEVPLIFDPTVKEDLNTDFKCVATNPRSPQSILHTYKE 326

```

RESULT 11

S30444 SIZ protein - human

C:Species: Homo sapiens (man)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000

C:Accession: S30444

R.Tominaga, S.; Yokota, T.; Yanggiasawa, K.; Tsukamoto, T.; Takagi, T.; Tetsuka, T.

Biochim. Biophys. Acta 1171, 215-218, 1992

A:Title: Nucleotide sequence of a complementary DNA for human ST2.

A:Reference number: S30444; MUID:93129624; PMID:1482686

A:Accession: S30444

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-328 <TEXT>

A:Cross-references: EMBL:D12763; NID:G220076; PIDN:BA02233.1; PID:G220077

C:Superfamily: vaccinia virus B1SR protein; immunoglobulin homology

Query Match 6.3%; Score 229.5; DB 2; Length 328;

Best Local Similarity 23.7%; Pred. No. 1.2e-09;

Matches 81; Conservative 56; Mismatches 148; Indels 57; Gaps 11;

27 WGLTMRQIQVPEDEPAIKCPLEPHFLKFNYSHTAHSGTLTLYWTRQDDLEPINF 86

25 WGL-----ENELIVRCP-----ROGKPSYVDWYYSQYKSI--PTQER 62

87 LPENRISKEDVLMFRPTLNDYGNVTCMLNRTYCSKVAPELEVQDSCFNSPMKLPV 146

63 ---NRFPASGGLKRLPAEVDASGITYCIVASPTFRNGYANVTYKQSDCNVD----- 115

147 HKLYIEYCI-----QRITCPNDVGPSSVKTPTTYMGCKYIQNFNNVPEGANLSF 199

116 ---YLMSTVGSGSEKNSKIYCEPTIDLY---NMTAPLEWFKNQALQGSR---YRAHKS 165

200 LI-----ALISNNQNTCVVTPYENGRTFHLTLTYKVVGSRKNAVPTIHPNDHVTYK 256

166 LVINNVMTEDAGDYCKEPIHNENGNANVSATRSFTVDEOGFSLEPIGAPAOKEIIEV 225

257 ERGEELIPCTVYVPSFLMDSRNEVMTIDGKKPD-----ITIDVTINESISHRTDET 311

226 EIGKANLTCACRGCKGQFLAAVLMQANGKRTIDPGEPRIQDEGQNSNGLA---C 282

312 RTQILISIKVTSSEDLKSYCHASAKGEVAKAAVKOKVPA 353

283 LDMVLRIDVKEEDLLQDYDCLALNHLGRRHTVRLSRKNS 324

RESULT 12

Fit-1S protein precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 25-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 19-May-2000

C:Accession: S42632

R:Bergers, G.; Kellertorfer, A.; Braselmann, S.; Graninger, P.; Bueslinger, M.

EMBO J. 13, 1176-1188, 1994

A:Title: Alternative promoter usage of the Fos-responsive gene Fit-1 generates mRNA iso-

A:Reference number: S42632; MUID:94178260; PMID:8131748

A:Accession: S42632

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-336 <BER>

A:Cross-references: GB:U04319; NID:9488278; PIDN:AAA67172.1; PID:9488279

C:Superfamily: vaccinia virus B1SR protein; immunoglobulin homology

Query Match 6.0%; Score 220; DB 2; Length 336;

Best Local Similarity 23.5%; Pred. No. 6.6e-09;

Matches 91; Conservative 62; Mismatches 145; Indels 90; Gaps 18;

4 LMCV---VSLYFYGILOSASERCDDWGLDTRQIQVDEPAIKCPLEPHFLKFNYS 59

9 LMAALILVPMYFI---VTEGRKTSGL-----ENELIVRCP----- 43

60 TAAAGLTLIYWTRODLEPINFRLP---ENRISKEDVLMFRPTLNDYGNVTCML 116

44 ORGGAINEVEWYNSN-----TIERIPTQKRNRIFVSRDLKFLPAKVEDSGITYCVI 95

117 RNTTYCSKVAPELEVQK-DSCFNSPMKLPVHKLYIEG-----IQRTCPNDVGPSSV 171

96 RSPESIKTGSINVTYKRPNC-----KIPYMMSTVDSGSDKSKITCPTIAY--NW 147

172 KPTIYMGCKYIQNFNNVPE-GANLSFL-IALIS--NNGNYTCVVTYENGRTFHL-- 225

Db 148 TAPVQFENKCALQG-----PRFAHMSYLFIDKSHVDEGDTYCRFHTENGNTYIYTA 202

226 TRITTYKVSPPKNAVPPVHSPNDHVTYKEPEBELLIPTCYFSLMDSRNEVMTID 285

203 TRSFVEEKG---STPPVITNPPHNTYVEEIGKTNIAACAFGTASQFVAVM----- 255

286 GKDDDDITIDVTINESISHRTDE-----TRQILISIKVTSSEDLKRSYVCH 333

256 -----QINKTRIGSGKARIQDEKPNKSSNGMCLTSLARITGVTDKDPSTKIDCV 308

334 ARSAKGEVAKAAVKOKVPAARYVELA 361

309 AMNHGVIRHPVRLRRKQPSKECLSQIA 336

RESULT 13

B1SR protein precursor - vaccinia virus (strain WR)

C:Species: vaccinia virus

A:Note: host Homo sapiens (man)

C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Jun-2000

C:Accession: A38472; J00929

R:Smith, G.L.; Chan, Y.S.

J. Gen. Virol. 72, 511-518, 1991

A:Title: Two vaccinia virus proteins structurally related to the interleukin-1 recept

A:Reference number: A38472; MUID:91170931; PMID:1626022

A:Accession: A38472

A:Molecule type: DNA

A:Residues: 1-326 <SM1>

A:Cross-references: GB:U01018; NID:G222696; PIDN:BA00825.1; PID:G222697

C:Superfamily: vaccinia virus B1SR protein; immunoglobulin homology

C:Keywords: glycoprotein

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-326/Product: B1SR protein #status predicted <BRP>

F:41-101/Domain: immunoglobulin homology <IMM1>

F:136-196/Domain: immunoglobulin homology <IMM2>

F:235-311/Domain: immunoglobulin homology <IMM3>

F:48-99/143-194/242-309/Disulfide bonds: #status predicted

F:80/103/113/206/237/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 5.2%; Score 189; DB 1; Length 326;

Best Local Similarity 24.0%; Pred. No. 1.4e-06;

Matches 80; Conservative 60; Mismatches 156; Indels 38; Gaps 16;

8 VSLYFY-GILOSASERCDDWGLDTRQIQVDEPAIKCPLEPHFLKFNYSHTAHSG 66

9 LSIFVSSPQTFAPAPCIDKG-QYFASFMELENEPVILPCPOI-NLSSGYNI-----L 61

67 TLIYWTRODLEPINFRLPERRISKEDVLMFRPTLNDYGNVTCMLRNTYCSKVA 126

62 DILWEKRGANDRIIPID-----NGSNMLINLT-OSDSGIYICITTNETTCWMS 111

127 FPLEVQKDSCEFSNPKLPVHKLYIEYGIQRTCPNDVGFPSVKTPTTYMGCKYIQN 186

112 LNLTVSVSESNIDLSYF--QIVNERSGEMVCPNINAIASVANDIIM-SGHRRLR- 167

187 FNNVPEGMNLSFLIALISNN--GNVTCVVTYENGRTFHLTLTYKVVGSRKNAVPPV 244

168 -NKRLQRTFGIITIEVRRKNDAGYVCLVEIYGGTVAVTIVKLEV---RDKIIPST 223

245 IHPNDHVTYKEPEBELLIPTCYFSLMDSRN-EVMTIDGKKPDITIDVTINESIS 303

224 WQLPDGIYV---SIGSNLTACRV--SLRPPTDADVFWLSNGYVEEDDGNGRISVA 278

304 HSRTEDETR---TQILISIKVTSSEDLKRSYVCHA 334

279 NKIYMTDKRVIISRLNINPVKEED-ATPFTQMA 311

RESULT 14

interleukin-1 beta receptor - vaccinia virus (strain Ankara)

C:Species: vaccinia virus

```

1: IntJctns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 118
2: 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 30
3: 1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 5
Query Match
Best Local Similarity 21.6%, Pred. No. 7,3e-05;
Matches 141; Conservative 87; Mismatches 227; Indels 198; Gaps 39;
5.2%, Score 189; DB 2; Length 5175;
QY 72 WTRQDRDLEEDINFLPNRISKEKDVIMFRPTLLNDTNGNTYCMLENTTYCSKVAPELEV 131
DB 3515 WFRGDK-----PV-YLYDRYSISPDGSHITINAKSLDGGKTYICRASNEAGSTIDILTKI 3569
QY 132 -----VQDSCFNSPMKLPVHKLYIEYGIQRTCTGNVQGFSSVYKPTITWYMGCKYI-Q 185
DB 3570 LVPPKIDKSNITGNELAVARTYLE-----CP-ISGI-----DQPDVIMTKNGMDINN 3617
QY 186 NFNNVYIPGKMULSPLI--ALISNNNGYTCVVYYPENGRTFHLTRITLVYVWSPK---NA 240
DB 3618 TDSRVITLAQNNETFEIENVQVTDGSRITCTAT-ANGGKASH---DESLVLSPEEDIHG 3673
QY 241 VPPVISHPNHVVYEKEKEGEBELLIPCTVYFS-FLMDSRNEVWTTIDGKKRDDITIDVTIN 299
DB 3674 TQPTI-----KRGSDITTLTCPIKLAEDIADQVMDVSWTSDKSRALDG---DLTNN 3720
QY 300 ESISHSRTEDETRTQIILSIKVTYSEDLRKSYVYGHARSAKGEVAKAAKVKQKVP----- 352
DB 3721 VDIS-----DQGRKLTITQASLENNAGL---YTCIALMRAGEASLEPKVEILSPPVIDISR 3772
QY 353 ---APRYVE---LACGFGATVLLVILIVYVH---VYWMLEMLFYRANHGTDETTIID 401
DB 3773 NDVQGVAVANOPTIMRCA-----VTGHPPEPSIKMLK-----N 3804
QY 402 GKEXYDIYVSYARNAA--EEEFVLLTRGVLENEFGYKLCIFPDRDSLPGNTVEAVEPFIQ 459
DB 3805 GKE-----VTDDENIRIYVQGVQLQILR--TDSHAKGKMSVVAENDA--GVKELEMYVD--- 3854
QY 460 RSRRMIVLSPDYVTEKS---ISMLEFKLVGMCONSIAATKLIVBRYRPLEHHPHGILOLK 516
DB 3855 -----VFTEPPVVSVKSDNPIKALGETITTLFCNAS-----GNYP---QLK 3891
QY 517 -----ESVSEFVSMKGEKSKSHGSKKFKKALRLALP-LRSLAS-----SGWNSCSCSOSDIL 567
DB 3892 WAKGSLIFDSPPDGARISLKGA-----RLDIPHLKKTVDGDIYTCQALNAAGTSSEASVS 3945
QY 568 DHVQRRRSRLKEPPELOSSERAAGSPAPAGKMSKHGKSSATCCRCVYCSGEMHLRNS 627
DB 3946 D-----VAVPEPI-NRDGIDMSFRP-----AQSSTLQIC---LAQG----- 3978
QY 628 RAEIHNDQWETHLCKPVPOSETWIONGTRELEBPAPQISALALHHFTDLSN 680
DB 3979 -----KPVPO---MRWTLNGTALTSTPQITVAASDSTFIQINN 4013
Search completed: April 23, 2003, 08:54:58
Job time : 56 secs

```


GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 23, 2003, 08:44:25 ; Search time 27 Seconds

(without alignments)
1055.342 Million cell updates/sec

Title: US-10-061-727-2

Perfect score: 3669
Sequence: 1 MTLMLCVSLYFYGLQSDA.....SALALHFTDLSNNNDPYIL 687

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

ched: 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	493.5	13.5	ILIR_RAT	002955 rattus norv
2	484.5	13.2	ILIR_MOUSE	P13504 mus musculu
3	424.5	11.6	ILIR_HUMAN	P14780 homo sapien
4	314	8.6	ILIS_MOUSE	P27931 mus musculu
5	302	8.2	ILIS_RAT	P43303 rattus norv
6	261	7.1	ILIS_CERAT	Q29612 ceropithec
7	252	6.9	ILIS_HUMAN	P27930 homo sapien
8	230.5	6.3	IRLI_MOUSE	P14719 mus musculu
9	229.5	6.3	IRLI_HUMAN	Q01638 homo sapien
10	189	5.2	VB16_VACCV	P25132 vaccinia vl
11	187	5.1	VB16_COMPR	Q04523 compox viru
12	182	5.0	VB16_VACCC	P21116 vaccinia vl
13	174	4.7	TLR1_MOUSE	Q99PQ1 mus musculu
14	164	4.5	TLR2_HUMAN	Q06003 homo sapien
15	163.5	4.5	TLR6_HUMAN	Q9Y2C9 homo sapien
16	161.5	4.4	TLR6_MOUSE	Q96W9 mus musculu
17	159	4.3	TLR2_CHICK	P08953 drosophila
18	154.5	4.2	TLR2_CHICK	Q96D66 gallus gall
19	153	4.2	TLR2_MACFA	Q95M53 macaca fasc
20	151.5	4.1	MY88_MOUSE	P22366 mus musculu
21	148.5	4.0	CAML_MOUSE	P11627 mus musculu
22	147.5	4.0	TLR1_HUMAN	P15399 homo sapien
23	147	4.0	TLR7_MOUSE	P58681 mus musculu
24	145	4.0	TLR2_BOVIN	Q951A9 bos taurus
25	143.5	3.9	TLR4_HUMAN	Q00206 homo sapien
26	142.5	3.9	TLR4_PAPAN	Q9TSP2 papio anubi
27	142.5	3.9	TLR4_PANPA	Q9TENO pan paniscu
28	141.5	3.9	TLR4_BOVIN	Q9G165 bos taurus
29	139	3.8	MY88_HUMAN	Q96336 homo sapien
30	138	3.8	TLR2_MOUSE	Q99UN7 mus musculu
31	138	3.8	TLR2_HUMAN	Q9BXT5 homo sapien
32	136.5	3.7	TL21_CHICK	Q96D78 gallus gall
33	136	3.7	KMLS_CHICK	P11799 gallus gall

34	135.5	3.7	1257	1	CAML_HUMAN	P32004 homo sapien
35	134	3.7	1284	1	NRCA_CHICK	P35331 gallus gall
36	133	3.6	1333	1	VGRI_MOUSE	P35969 mus musculu
37	133	3.6	2012	1	DSCA_HUMAN	O60469 homo sapien
38	132	3.6	784	1	TLR2_CRICR	Q91F8 cricetus
39	131.5	3.6	1259	1	CAML_RAT	O05695 rattus norv
40	130	3.5	1049	1	TLR7_HUMAN	O99YK1 homo sapien
41	129.5	3.5	819	1	FGRI_CHICK	P21804 gallus gall
42	129	3.5	808	1	FGRI_MOUSE	Q03142 mus musculu
43	129	3.5	822	1	FGRI_RAT	O04589 rattus norv
44	128	3.5	822	1	FGRI_HUMAN	P13362 homo sapien
45	127.5	3.5	823	1	CEK3_CHICK	P18461 gallus gall

ALIGNMENTS

RESULT 1	ID	ILIR_RAT	STANDARD:	PRT:	576 AA.
AC	002955;	ILIR_RAT			
DT	01-JUL-1993 (Rel. 26, Created)				
DT	15-JUN-2002 (Rel. 41, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Interleukin-1 receptor, type I precursor (IL-1R-1) (P80).				
GN	ILIR1 OR IL1RA.				
OS	Rattus norvegicus (Rat).				
OC	Burkholderia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_Taxid=10116;				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Ganglion;				
RX	MEDLINE=93266794; PubMed=7684399;				
RA	Hart R.P., Liu C., Shadick A.M., McCormack R.J., Jonakait G.M.;				
RT	"An mRNA homologous to interleukin-1 receptor type I is expressed in				
RT	cultured rat sympathetic ganglia.";				
RL	J. Neuroimmunol. 44:49-56(1993).				
CC	-1- FUNCTION: RECEPTOR FOR INTERLEUKIN-1 ALPHA (IL-1A), BETA (IL-1B),				
CC	AND INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN (IL-1RA). BINDING TO				
CC	THE AGONIST LEADS TO THE ACTIVATION OF NF-KAPPA B.				
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	-1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.				
CC	-1- SIMILARITY: CONTAINS 1 TIR DOMAIN.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
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CC	or send an email to license@sib-sib.ch).				
CC	-----				
DR	EMBL; M95578; AAA16196.1; ALT_SEQ.				
DR	HSSP; P14778; IL1RA.				
DR	InterPro: IPR004076; ILIR_receptor.				
DR	InterPro: IPR004075; ILI_receptor.				
DR	InterPro: IPR004074; ILI_receptor1/II.				
DR	InterPro: IPR003006; IG_MHC.				
DR	InterPro: IPR003600; IG_1like.				
DR	InterPro: IPR000157; TIR_domain.				
DR	Pfam; PF00047; ig; 2.				
DR	Pfam; PF01582; TIR; 1.				
DR	PRINTS; PRO1538; INTRLEUKINR1.				
DR	PRINTS; PRO1536; INTRLEUKINR12F.				
DR	PRINTS; PRO1537; INTRLEUKINR1F.				
DR	SMART; SM00410; IG_1like; 1.				
DR	SMART; SM00255; TIR; 1.				
DR	PROSITE; PS50104; TIR; 1.				
KW	Immunoglobulin domain; Receptor; Glycoprotein; Transmembrane; Signal;				
KW	Repeat; Phosphorylation.				
FT	SIGNAL	1	19		BY SIMILARITY.
FT	CHAIN	20	576		INTERLEUKIN-1 RECEPTOR, TYPE I.


```

FT DOMAIN 20 338 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 339 359 POTENTIAL.
FT DOMAIN 360 576 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 39 113 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 138 206 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 244 322 IG-LIKE C2-TYPE DOMAIN 3.
FT DOMAIN 386 544 TIR.
FT DISULFID 25 107 BY SIMILARITY.
FT DISULFID 46 99 BY SIMILARITY.
FT DISULFID 145 199 BY SIMILARITY.
FT DISULFID 251 315 BY SIMILARITY.
FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 236 236 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD RES 556 556 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
SQ SEQUENCE 576 AA; 66758 MW; 55B20C92385A34A CRC64;

Query Match 13.5%; Score 493.5; DB 1; Length 576;
Best Local Similarity 26.5%; Pred. No. 7.6e-30;
Matches 153; Conservative 105; Mismatches 230; Indels 89; Gaps 25;

47 CPLEFHEFKYVSTAHSAGLTLVYWTRODRDLEPINFLPENRISKEKQVLMFRPFL 106
46 CPLEFHEFKYVSTAHSAGLTLVYWTRODRDLEPINFLPENRISKEKQVLMFRPFL 91
107 NDTGNTYTMRLNTYCSKVAPELVQKDS--CFNSPMKLVHKLVEYGIQITCPND 164
92 EDGYYCYIMNSNTYCKTKITMSVLENDPCLCYNTQASF-IQLHVA-GDGSIVCEYLD 149
165 GYF--PSVYPTITWNGCKIQFNPNVIBEGMLSFILALISNN-----GNTCVTY 216
150 -FPDENNELPKQWYKNCPLP-----LDDGNFGFKNKLWVNAEHRGNTVCRTSY 203
217 PENCRTFLTRTLTVKVGSPKNAVPPVHSPNDVYVEKEGELLIPCTVYFSFLMDS 276
204 TYGCKQVPTVITVITITIDSKRP-REVINSRHEM-EDPRSTIQLICNVTOF---- 257
277 RNEVWMTIDGKPD-DITIDVTINESISH-SRTEDETRTOILSIKYSEDLKRSYVCHA 334
258 TDLYVWKMNGSEIEMDDPILEDYQFLEHPSAKKTYLITLANSVYKGYRYPFCV 317
335 RSKAGEVAAKAKYKQKPPARYTVELACGRATLVILIVHYVYVLEWLYTPRAFG 394
318 KNT--HILETAHVLVYPVDPFNKYLIGFAITATVAFCAICYKVFVDIVLWYRSCS 375
395 --TDETLIDGKEYDIYVSANAAE-----EEFVLLTLRGVLENEFGYKLCIFDRSLP 446
376 DFLPKRKSADGRTYAVLYLPTKTEGSGFAYIDTVPKLLPEVLGQFGYKLFICGRDYV 435
447 GGNTEAVDFEIQSRNRNVIVLSPDYVTEKSIIMLEFK-LGWMCONSIA-----TK 496
436 GEDTIEVTNENVKSRRLIILVRD-----MGSEFCLOSGSEBOIAIYDALIREGIK 487
497 LIVVEYRPLEPHPCIIQKESVSFVS-----WKG---EKSHSGSKFKKARLALPL 546
488 IILELEKIOEY---KMPESIOFIKQKGAICWSDGFKRPSAKTRFWKNLRYOMPA 543
547 RSLASAGSNSSGSSQSDISLDHYORRRSRLEKPEL 583
544 QRS-----PLSGHLLITLDPVLDTEKQIAETHL 573

RESULT 2
ILIR MOUSE STANDARD; PRT; 576 AA.
ID ILIR MOUSE
AC P13504;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-1 receptor, type I precursor (IL-1R-1) (P80).
ILIR1 OR ILIRA OR IL-IR1.

```

```

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RX SEQUENCE FROM N.A., AND SEQUENCE OF 20-45.
RA MEDLINE=88290679; PubMed=2969618;
RA Sims J.B., March C.J., Cosman D., Widmer M.B., McDonald H.R.,
RA McMahon C.J., Grubin C.B., Wiggall J.M., Jackson J.L., Call S.M.,
RA Friend D., Alpert A.R., Gillis S., Urdal D.L., Dower S.K.,
RA "cDNA expression cloning of the IL-1 receptor, a member of the
RA immunoglobulin superfamily."
RA Science 241:585-589(1988).
RL [2]
RP PHOSPHORYLATION OF THR-556.
RX MEDLINE=91254338; PubMed=1828344;
RA Bird T.A., Woodward A., Jackson J.L., Dower S.K., Sims J.B.,
RA "Phorbol ester induces phosphorylation of the 80 kilodalton murine
RA interleukin 1 receptor at a single threonine residue."
RA Biochem. Biophys. Res. Commun. 177:61-67(1991).
RL [3]
RL FUNCTION: RECEPTOR FOR INTERLEUKIN-1 ALPHA (IL-1A), BETA (IL-1B)
AND INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN (IL-1RA). BINDING TO
CC THE AGONIST LEADS TO THE ACTIVATION OF NF-KAPPA B.
CC [4]
CC SUBCELLULAR LOCATION: Type I membrane protein.
CC [5]
CC SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC [6]
CC SIMILARITY: CONTAINS 1 TIR DOMAIN.
CC [7]
CC THIS SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC [8]
CC EMBL; M20658; AAA39279.1; -.
CC PIR; A32604; A32604.
CC HSSP; P14778; ILIR.
CC MGD; MG196545; ILIR1.
CC InterPro; IPR004076; ILIR_receptor.
CC InterPro; IPR004075; IL1_receptorI.
CC InterPro; IPR004074; IL1_receptorII.
CC InterPro; IPR003006; IG_MHC.
CC InterPro; IPR003600; IG_Like.
CC InterPro; IPR000157; TIR_domain.
CC Pfam; PF00047; IG_2.
CC Pfam; PF01582; IG_1.
CC PRINTS; PRO1538; INTRLEUKNIR1.
CC PRINTS; PRO1536; INTRLEUKNIR2P.
CC PRINTS; PRO1537; INTRLEUKNIRF.
CC SMART; SM00410; IG_Like; 1.
CC SMART; SM00255; TIR; 1.
CC PROSITE; PS01004; TIR; 1.
CC Immunoglobulin domain; Receptor; Glycoprotein; Transmembrane; Signal;
CC Repeat; Phosphorylation.
CC [9]
CC SIGNAL 1 19
CC CHAIN 20 576
CC DOMAIN 20 338
CC TRANSMEM 339 359
CC DOMAIN 360 576
CC DOMAIN 39 113
CC DOMAIN 138 206
CC DOMAIN 244 322
CC DOMAIN 386 544
CC DISULFID 25 107
CC DISULFID 46 99
CC DISULFID 145 199
CC DISULFID 251 315
CC CARBOHYD 63 63
CC CARBOHYD 103 103
CC CARBOHYD 236 236
CC CARBOHYD 252 252

INTERLEUKIN-1 RECEPTOR, TYPE I.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
IG-LIKE C2-TYPE DOMAIN 3.
TIR.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOD RES 556 556 PHOSPHORYLATION (BY PKC).
 SQ SEQUENCE 576 AA; 66697 MW; 7AA8304C86412A16 CRC64;
 Query Match 13.2%; Score 484.5; DB 1; Length 576;
 Best Local Similarity 25.8%; Pred. No. 3,7e-29;
 Matches 153; Conservative 120; Mismatches 225; Indels 95; Gaps 27;
 QY 34 QIOVFEDDEPARI-----KCPLEHFKFNSTASHASAGLILVITWTRDRLLE 81
 DB 21 EIDCTYPMQIVLFLSVNEIDIRKCPYPRKMH-----GDTIIWY---KNDST 67
 QY 82 PINRLPENRISKEKDVLMFEPRLNDTGNATLQALNTTYSKVAFLLEVYOKS---CFN 139
 DB 68 PISAD-RDSNTHOONHELMFPAVEDSGTYCYLVNSTYTLKTKVTVLENDPGLCYG 126
 DB 140 SPMLPVHKLVIEXGIRITCPNDGYF--PSSVKPTITWYMGCKYIQNFNNTVPEGMT 197
 DB 127 TQATFP-ORLHIA-GDCSLVCPYV-SYFKDENNELPEVQYKNC-KPILLDNVSGVVD 182
 QY 198 SPFLALIS--NNGNYTCVATYTPENGRTFLTRITLVKVGSPKAVPVVHSPMDHYVE 255
 DB 183 KLVIRNVAEHRGDIYGRMSYTFRGKQYPTVRIQTITDENKRD-RPVILSPENETI-E 240
 QY 256 KEPGEELLICTVYFSLDMSRNEWMTIDGKPDITDITVINES-----ISHRT 307
 DB 241 ADPSMQLICNVYTGQF---SDLVYKKNMS-----EEMWDPLAEDYQVEHPST 289
 QY 308 EDE-TRTQILSIKKVTSSEDLKRSVYCHASAGKAVAKVOKVAPARYVELACGFGA 366
 DB 290 KKKYTLITLITNISVKSQFRYPFICVVKNT--NIFSAHQVLYPVPDRFNVLYIGFTI 347
 QY 367 TVLLVVLIVVHYVYLMVLEMLFPAHNG--TDETLIDGKEYDIVSYARNAE-----B 418
 DB 348 LRTATVCCVCIYKFKVDIVLWYRDSGSGFLPSKASDGKTYDAVILPKTLGSGSPFDLD 407
 QY 419 EPLLTLRGVLENGRGYKLCIFDRDLSLPGNTVAVAVDFIORSRMTVLSPLD----- 471
 DB 408 TFPFKLPVLEVGQFKLTYGDDYVGGDTLEVTNENWKSRLILILVRDMGFSWL 467
 QY 472 -VYTESKISMLFPLGVMCONSIATKLIIVEYRPLE--HHPGIIQ-LKESVSFVSKG- 526
 DB 468 GQSEEGIAL-----YNMLIGGI-KIVLLELEKIDQYEMKPSIQIKKHGIVICMSGD 521
 DB 527 --EKSKHSGSKFKARLALPLASLSAGSGNESCQSQSDISLDHVRRSRL 577
 DB 522 FOERPOSAKTRFWKNLYOMPAQRSS-----PLSKRRLTLDPVADTEKL 567
 RESULT 3
 ILIR HUMAN STANDARD; PRT; 569 AA.
 ID ILIR HUMAN
 AC P14778;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-1 receptor, type I precursor (IL-1R-1) (IL-1R-alpha)
 DE (P80) (Antigen CD121a).
 GN ILIR1 OR ILIRA OR ILIR.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=90098789; PubMed=2533321;
 RA Chua A.O., Gubler U.;
 RT "Sequence of the cDNA for the human fibroblast type interleukin-1
 receptor.";
 RL Nucleic Acids Res. 17:10114-10114(1989).
 RN (2)

RP SEQUENCE FROM N.A.
 RC TISSUE=T-cell;
 RX MEDLINE=90046906; PubMed=2530587;
 RA Sims J.E., Acres R.B., Grubin C.E., McMahon C.J., Wignall J.M.,
 RA March C.J., Dower S.K.;
 RT "Cloning the Interleukin-1 receptor from human T cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8946-8950(1989).
 RN (3)
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 18-332 IN COMPLEX WITH IL1B.
 RX MEDLINE=97215903; PubMed=9062193;
 RA Vigers G.P., Anderson L.J., Caffes P., Brandhuber B.J.;
 RT "Crystal structure of the type-1 interleukin-1 receptor complexed
 with interleukin-1beta.";
 RL Nature 386:190-194(1997).
 RN (4)
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 21-331 IN COMPLEX WITH IL1RA.
 RX MEDLINE=97215904; PubMed=9062194;
 RA Schreuder H., Tardif C., Trump-Kallmeyer S., Soffientini A.,
 RA Sarubbi E., Akesson A., Bowlin T., Yanofsky S., Barrett R.W.;
 RT "A new cytokine-receptor binding mode revealed by the crystal
 structure of the IL-1 receptor with an antagonist.";
 RL Nature 386:194-200(1997).
 CC - FUNCTION: RECEPTOR FOR INTERLEUKIN-1 ALPHA (IL-1A), BETA (IL-1B),
 CC AND INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN (IL-1RA). BINDING TO
 CC THE AGONIST LEADS TO THE ACTIVATION OF NF-KAPPA B.
 CC - SUBCELLULAR LOCATION: Type I membrane protein.
 CC - SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC - SIMILARITY: CONTAINS 1 TIR DOMAIN.
 CC - DATABASE: NAME=PROW; NOTE=CD guide CD121a entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd121a.htm".
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 CC -----
 CC EMBL; X16896; CAA34773.1; -
 DR EMBL; M27492; AAB59137.1; -
 DR PIR; S06928; S06928.
 DR PIR; A36187; A36187.
 DR PDB; 1IRB; 04-PEB-98.
 DR PDB; 1IRA; 17-JUN-98.
 DR GeneW; HGNC:5993; ILIR1.
 DR MIM; 147810; -
 DR InterPro; IPR004076; ILIR_receptor.
 DR InterPro; IPR004075; IL1_receptor1.
 DR InterPro; IPR004074; IL1_receptor1/1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003600; IG_Like.
 DR InterPro; IPR000157; TIR_domain.
 DR Pfam; PF00047; Ig_2.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PRO1538; INTERLEUKIN1.
 DR PRINTS; PRO1536; INTERLEUKIN1F.
 DR PRINTS; PRO1537; INTERLEUKIN1F.
 DR SMART; SM00410; IG_Like; 1.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PSS0104; TIR; 1.
 KW Immunoglobulin domain; Transmembrane; Glycoprotein; Receptor; Signal;
 KW Repeat; 3D-structure.
 FT SIGNAL 1 17
 FT CHAIN 18 569 INTERLEUKIN-1 RECEPTOR, TYPE 1.
 FT DOMAIN 18 336 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 337 356 POTENTIAL.
 FT DOMAIN 357 569 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 37 103 IG-LIKE C2-TYPE DOMAIN 1.
 FT DOMAIN 135 203 IG-LIKE C2-TYPE DOMAIN 2.
 FT DOMAIN 241 319 IG-LIKE C2-TYPE DOMAIN 3.
 FT DOMAIN 383 541 TIR.
 FT DISULFID 23 104

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FT DISULFID 44 96
FT DISULFID 121 164
FT DISULFID 142 196
FT DISULFID 248 312
FT CARBOHYD 100 100
FT CARBOHYD 193 193
FT CARBOHYD 233 233
FT CARBOHYD 249 249
FT CARBOHYD 263 263
FT CARBOHYD 297 297
SQ SEQUENCE 569 AA; 65402 MW; 5BAA83F8F0225C25 CRC64;

Query Match 11.6%; Score 424.5; DB 1; Length 569;
Best Local Similarity 24.3%; Pred. No. 1.3e-24;
Matches 129; Conservative 117; Mismatches 205; Indels 79; Gaps 24;

OY 67 TLIAWTRDRODLEERINERLEPENRISKEDVLMFRPTLLNDGNTYCMLENTYCSKVA 126
DB 54 TITWT-----KDSKTPVSTB-QASRIHOKEXLMFPAVEDSGHYCVVRNSYCLRIK 108
OY 127 PPLEVVOKDS--CFNS---PMKLPVHKLIEYGIORITCPNVGYF--PSSVKEPTTWY 178
OY 109 ISAKFVENEPNLCYNAQALFKQGLPV-----AGDGLVCPYME--PFKXNNELPGLQWY 161
OY 179 MGCYKIQNNVYIPEGMNLFLIALIS--NNGVYTCVVYYPENGRTFHLTRTLIVKVGVS 236
DB 162 KDC-KPLLDINHFSGVKORLLVMNVAEKRGNYTHASITYGKQYPTITRIVLEPTLEE 220
OY 237 PGNAAVPVHISPNDAHYEKEPEGEELLIPCTVYFSELMDSRNEVMWTTIDCKPDITIDV 296
DB 221 NKPTRPVIVSPANB--TMEVDLCSQIOLICNTYGOL-----SDIAYKKNMSVIDE--DDP 272
OY 297 TINESI---SHSRTEDETRTQIISTIKVTSSEDLKRSYVGHARSAGEVAKAKVKKQVP 352
DB 273 VIGBOYVSVENPANKRSRTLITVLANISIESREYKHPFCFAKNTG--IDAAYIQLIYV 330
OY 353 ARYVVELACGATVLLVYL--IVVHVYVLEVMVLPFR--AHGCTDETLIDGEXYDI 407
DB 331 VTNFOKHM---IGICVTLTVIIVCSVPYIKIFKIDIVLMWRDSQYPLPKASDGKTYDA 387
OY 408 VYSVARNABE-----EEFVLLTRGVLNEFGYKLCIFPDRLSPGANTVEAVFDIORS 461
DB 388 YLIPKPTVEGSDCDIVFKPLPREVLEKQCGYKLPYGRDDYVEDIVVENAVKXS 447
OY 462 REMIVVLSPDY-----VTEKSIEMLEFKLGVMCQNSIATYKLIVEXRPLEHPHGLI 513
DB 448 RLIIITLVRETSGFWMGSSSEQIAM---YNALVODGI--KVLLLELEKIDYR----- 497
OY 514 QKESEVSFVS-----WIGERS---KHSGSKFWKALRLALPKRSLSASS 553
DB 498 KPESEIKFKOKHGAIRMSGDFTQPOSASAKTRFMKVRVHMPVORRSPSS 547

RESULT 4
ILIS_MOUSE STANDARD; PRT; 410 AA.
AC P27931;
DB 01-AUG-1992 (Rel. 23, Created)
DB 01-AUG-1992 (Rel. 23, Last sequence update)
DB 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-1 receptor, type II precursor (IL-1R-2).
GN IL1R2 OR IL1RB OR IL-1R2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92007725; PubMed=1833184;
RA McMahon L.J., Slack J.L., Mosley B., Cosman D., Lupton S.D.,
RA Bruntun L.J., Grubin C.E., Wignall J.M., Jenkins N.A., Brannan C.I.,
RA Copeland N.G., Hübner K., Croce C.M., Cannizzaro L.A., Benjamin D.,
RA Dower S.K., Spriggs M.K., Sims J.E.;

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RT "A novel IL-1 receptor, cloned from B cells by mammalian expression,
RT is expressed in many cell types.";
RL EMBL J. 10:2821-2832 (1991).
CC -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-1 ALPHA (IL-1A), BETA (IL-1B),
CC AND INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN (IL-1RA).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
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CC -----
DR EMBL; X59769; CAA42440.1; -.
DR MGI; MGI:96546; IL1R2.
DR InterPro; IPR004074; IL1_receptor/I1.
DR InterPro; IPR004077; IL1_receptor/I1P.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_3.
DR PRINTS; PR01539; INTERLEUKIN1R2.
DR PRINTS; PR01536; INTERLEUKIN1R2F.
DR SMART; SM00409; IG_3.
DR K0 Immunoglobulin domain; Receptor; Glycoprotein; Transmembrane; Signal;
KW Repeat.
FT SIGNAL 1 13
FT CHAIN 14 410
FT DOMAIN 14 355
FT TRANSMEM 356 381
FT DOMAIN 382 410
FT DOMAIN 57 127
FT DOMAIN 157 226
FT DOMAIN 263 345
FT DISULFID 64 120
FT DISULFID 164 219
FT DISULFID 270 338
FT CARBOHYD 124 124
FT CARBOHYD 208 208
FT CARBOHYD 231 231
FT CARBOHYD 289 289
SQ SEQUENCE 410 AA; 45645 MW; 923DFC27C70AF604 CRC64;

Query Match 8.6%; Score 314; DB 1; Length 410;
Best Local Similarity 25.3%; Pred. No. 2.1e-16;
Matches 102; Conservative 73; Mismatches 164; Indels 64; Gaps 17;

OY 22 EKCDDMGIDTRQIOVDFDEPARIKCPLEFHLKNVSTASHAGITLIMWTRDRODLEB 81
DB 40 DNCQFRGREFKSELRL-GEEPVLMKCPILAPH---SDISSHSFLLT---MSKLSQOLI 91
OY 82 PINFLPENRISKEDVLMFRPTLLNDGNTYCMLENTYCSKVAPELVVOKDSCFNSP 141
DB 92 PRD-----EPRMVMKGNIMILIPAVQDSDGTIYCTFRNASHCEQMSVELKVF-----NTE 142
OY 142 MCLPVHKLIEYGIORIT---CPNVDSYFPSSVKEPTITWTMGCKYKIQNNVYIPEGMNL 197
DB 143 ASLP-HVSYLQISALSTGLVACPDLKEFISNADGKIQWYGA-----ILDKGNK 193
OY 198 SFLIA-----LISNN-----GNVTCVVYYPENGRTFHLTRTLIVKVGSPGNAAVPVYH 246
DB 194 EFLSGADPTLLIISTSDADAGYRCVMFTFYNGEYITRILKVGITTEPI-PVIL 252
OY 247 SPNDVHYEKEPEGEELLIPCTVYFSELMDSRNEVMWTTIDGKKPDITIDVINESISHSR 306
DB 253 SPLFTI--PASIGSLIAPCKVFLCTGTSNITVWMLNSPISAAVPRGRVTEGLHQQY 310
OY 307 TE-DETRTOI-LSIKVTSSEDLKRSYVGHARSAGEVAKAKVKKQVPAKRTVVLACGF 364
DB 311 SENDEVVEVSLIPFVTRDELDTDFKCVASNPSSQSISLHTTVKESVSFWSIALA--- 367

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QY 365 GATVLLVILVYHYVWLEMTLFTYRAHGTDTILDGKEYDI 407
DB 368 ---PLSLIILVV---GAIMWRRCRRA-----GKTYGL 395

RESULT 5
ID IL1S_RAT STANDARD; PRT; 416 AA.
AC P43303;
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 41, Last annotation update)
DE Interleukin-1 receptor, type II precursor (IL-1R-2).
GN IL1R2 OR IL1RB OR IL-1R2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
(1)
RP SEQUENCE FROM N.A.
RX MEDLINE=95035882; PubMed=7524717;
RA Brisulf J., Gatti S., Malinowsky D., Bjork L., Sundgren A.K.,
RA Bartal T.;
RT "Interleukin-1 stimulates the expression of type I and type II
RT interleukin-1 receptors in the rat insulinoma cell line R1mSP;
RT sequencing a rat type II interleukin-1 receptor cDNA.";
RL Eur. Cytokine Netw. 5:319-330(1994).
CC -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-1 ALPHA (IL-1A), BETA (IL-1B),
CC AND INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN (IL-1RA).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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CC
DR EMBL, Z22812; CAA80465.1;
DR InterPro; IPR004074; IL1_receptor/IL1.
DR InterPro; IPR004077; IL1_receptor/IL1.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; ig_3.
UR PRINTS; PRO1539; INTERLEUKIN12.
UR PRINTS; PRO1536; INTERLEUKIN12F.
DR SMART; SM00409; IG_3.
KW Immunoglobulin domain; Receptor; Glycoprotein; Transmembrane; Signal;
KW Repeat.
FT SIGNAL 1 13 POTENTIAL.
FT CHAIN 14 416 INTERLEUKIN-1 RECEPTOR, TYPE II.
FT DOMAIN 14 355 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 356 381 POTENTIAL.
FT DOMAIN 382 416 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 57 127 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 157 226 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 263 345 IG-LIKE C2-TYPE DOMAIN 3.
FT DISULFID 64 120 BY SIMILARITY.
FT DISULFID 164 219 BY SIMILARITY.
FT DISULFID 270 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 124 208 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 208 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 231 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 46353 MW; 50EFBA4881C5D4E CRC64;
SQ SEQUENCE 416 AA; 46353 MW; 50EFBA4881C5D4E CRC64;

Query Match 8 2% Score 302; DB 1; Length 416;
Best Local Similarity 25.3%; Pred. No. 1,7e-15;
Matches 97; Conservative 67; Mismatches 153; Indels 66; Gaps 18;
QY 25 DDW--GLDTRQIOVEDPARIKCPLEFHEFLKFNYSSTAHSAGLTLIWTYTRQDRDLEEP 82

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DB 41 DCWFRGRDRKSELR.L-EGEPVILRCPLVPH-----SDTSSSSRSL-L-TWSKSDSOLIP 92
QY 83 INFRLEPNRISKQVILWRPILNDTGNVTCMLANTNTYCSVAPAFLEVVQDSCFNPM 142
DB 93 GD---EPRMVKADDTLWVLPVAVQDQSGTYICTFRNASHCEQWSELEKVKF-----NTRA 143
QY 143 KLPVHKLYIEYGIQRT-----CPNVGYPPSSVSKPTTYWMCYKIQNFNNVYPEGNNLS 198
DB 144 SPFLVS-VIQISALSTGLVCPDLKEFISRTDQKIQYK-----SILDGKNNK 194
QY 199 FLIA-----LISNN-----GNVTCVYTPENGRTFHLTRLLTVKVSPPKAVPVIHS 247
DB 195 FLGADPTRLILSNITSMGADGYRCVMTFTYEGKEVITRNIELRVKGIITTEPI-FVILS 253
QY 248 PDNVHYEKEPEBELIPTCTVPSFLMOSRNWVWTTIDSKRDDITIDVT-----INESI 302
DB 254 PLETTI--PASLSRLVLPCKVFLGTGTSNTIYVW-----MANSTFISVAYPRGRYTEGL 306
QY 303 SHSRTE-DETRTQI--LSIKVTSBDLKRSYVCHASAKGEVAKAKVKQVPAPRYVEL 360
DB 307 HNOYSNDENVYEVSLIPPTVKEDLNDTRKCVATNPRFSQHLHTVKE-----VSS 358
QY 361 ACQFGATVLLVILVYHYVWL 383
DB 359 TFSWGIALPLSLIILVVGAIWI 381

RESULT 6
ID IL1S_CERAB STANDARD; PRT; 393 AA.
AC Q29612;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-1 receptor, type II precursor (IL-1R-2) (IL-1R-beta).
GN IL1R2 OR IL1RB.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Cercopithecus.
OC NCBI_TaxID=9534;
(1)
RP SEQUENCE FROM N.A., AND SEQUENCE OF 125-145.
RX MEDLINE=96355446; PubMed=8702856;
RA Liu C., Hart R.P., Liu X.J., Clevenger W., Maki R.A., Souza E.B.;
RT "Cloning and characterization of an alternatively processed human
RT type II interleukin-1 receptor mRNA.";
RL J. Biol. Chem. 271:20965-20972(1996).
CC -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-1 ALPHA (IL-1A), BETA
CC (IL-1B), AND INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN (IL-1RA).
CC -1- SUBCELLULAR LOCATION: THE LONG ISOFORM IS A TYPE I MEMBRANE
CC PROTEIN WHILE THE SHORT ISOFORM IS SOLUBLE.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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CC
DR EMBL, U64092; AAB05876.1;
DR EMBL; U64093; AAB05877.1;
DR HSSP; P14778; IIRB.
DR InterPro; IPR004074; IL1_receptor/IL1.
DR InterPro; IPR004077; IL1_receptor/IL1.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003600; IG_Like.

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PFam: PF00047; ig: 3.
 DR PRINTS; PRO1539; INTERLEUKINR2.
 DR PRINTS; PRO1536; INTRLEUKINR12P.
 DR SMART; SM00409; IG: 2.
 DR SMART; SM00410; IG: 1like; 1.
 DR Immunoglobulin domain; Receptor; Glycoprotein; Transmembrane; Signal;
 KW Repeat; Alternative splicing.
 FT SIGNAL 1 13 POTENTIAL.
 FT CHAIN 14 393 INTERLEUKIN-1 RECEPTOR, TYPE II.
 FT DOMAIN 14 347 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 348 368 POTENTIAL.
 FT DOMAIN 369 393 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 43 115 IG-LIKE C2-TYPE DOMAIN 1.
 FT DOMAIN 145 214 IG-LIKE C2-TYPE DOMAIN 2.
 FT DOMAIN 251 333 IG-LIKE C2-TYPE DOMAIN 3.
 FT DISULFID 50 108 BY SIMILARITY.
 FT DISULFID 152 207 BY SIMILARITY.
 FT DISULFID 258 326 BY SIMILARITY.
 FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 219 219 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 297 393 MISSING (IN SHORT ISOFORM).
 SQ SEQUENCE 393 AA; 44778 MW; D4D746C5DE569A8 CRC64;
 Query Match 7.1%; Score 261; DB 1; Length 393;
 Best Local Similarity 21.9%; Pred. No. 2, 1e-12;
 Matches 89; Conservative 64; Mismatches 185; Indels 68; Gaps 15;
 QY 20 ASERCDWGLDTRQIOVEFDEPARIKCPLEHFLKKNYSTASAGLTLYMTROQRDL 79
 DB 24 AASCSVGRGHYKKEFL-EGEPVALKCPQ---VPYQLAASVPHNLWHRKDSARAV 78
 QY 80 --SEPIFRLEPNRISKEDVLFRRPTLADNGYTCMLNTYCSKVAPELVQKQSC 137
 DB 79 PGEE-----ETRMNQDGLMLPLALQSDSGYICTTNNASCDKVSLELAVFE---- 127
 QY 138 FNSPMKLPVHKLTYEY-----GIORITCPNVDSYPPSSVKEPTITWYGCYKIONFN 188
 DB 128 -NTDASLP-----FISYPOILTLSTFGV--LVCPDLREFTRDKTGKIQWYKDLPLDKDN 180
 QY 189 NVFPEGNNLSFLI---ALISNNNGYTVVYPPENGRTFHLTRTLTVKVVSPKNAVPEVI 245
 DB 181 EKPLSVGTGTHLLVHDVALDAGYRCVLPFHEGQOYNITRNLTELEIKKKKEETI--PVI 239
 QY 246 HSPNDHVVYEKEPEGEELLIPCTVYFSEFLMSRNEVMWITIDCKRPDDITIDVTINESISHS 305
 DB 240 ISPLKTI--SASLGSRLTIFCKVFLGTGTPLTLMWMTAN-----DTHVESAVPGG 288
 QY 306 RTEDETRTQI-----LSIKVYTSBDLKRSYVCHASAKGEVAKAKVKKVAP 354
 DB 289 RVEGPRQSESENENNYLEVPLIDPVRKIDNNVFCFNFVNTWGFOTLRITVVE--PPP 346
 QY 355 RYTYELACGPGATLVLLVIVVYHVYMLEVLFYRAHFGDEITL 400
 DB 347 TFS-----WGIVLAPLALFVLVGIWMHRRCKHRTGKADGLTVL 386
 RESULT 7
 ILIS_HUMAN STANDARD; PRT; 398 AA.
 AC P27930; Q9UB68;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-1 receptor, type II precursor (IL-1R-2) (IL-1R-beta)
 DE (anti-gen Cdb121b).
 GN IL1R2 OR IL1RB.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_Taxid=9606;
 FT

RM SEQUENCE FROM N.A.
 RP TISSUE-B-cell;
 RX MEDLINE=92007725; PubMed=1833184;
 RA McMahon C.J., Slack J.L., Mosley B., Cosman D., Lupton S.D.,
 RA Brunton L.L., Grubin C.E., Mignall J.M., Jenkins N.A., Brannan C.I.,
 RA Copeland N.G., Huebner K., Croce C.M., Cannizzaro L.A., Benjamin D.,
 RA Dower S.K., Spriegs M.K., Sime J.E.;
 RT "A novel IL-1 receptor, cloned from B cells by mammalian expression,
 RT is expressed in many cell types.";
 RL EMBO J. 10:2821-2832 (1991).
 [2]
 RM SEQUENCE FROM N.A.
 RP Chou H.-H., Takashiba T., Takigawa M., Maeda H., Asahara Y.,
 RA Nishimura F., Arai H., Murayama Y.;
 RT "Complete nucleotide sequence and expression of the human
 RT interleukin-1 receptor type II in human gingival fibroblasts.";
 RL Submitted (Oct-1996) to the EMBL/Genbank/DBJ databases.
 [3]
 RM SEQUENCE FROM N.A.
 RP Mead K., Maupin R., Yoakum M., Hotic M.;
 RT "The sequence of Homo sapiens BAC clone RP11-451C2.";
 RL Submitted (Mar-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-1 ALPHA (IL-1A), BETA (IL-1B),
 CC AND INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN (IL-1RA).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: CONTRAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- DATABASE: NAME=PROV; NOTE=CD guide CDW121B entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw121b.htm".
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 CC
 DR EMBL; X59770; CAA42441.1; -;
 DR EMBL; U74649; AAD00242.1; -;
 DR EMBL; AC007165; AAK52072.1; -;
 DR PIR; S17428; S17428.
 DR HSP; P14778; I1TB.
 DR Genew; HGNC:5994; IL1R2.
 DR MIM; 147811; -;
 DR InterPro; IPR004074; IL1_receptor/II.
 DR InterPro; IPR004077; IL1_receptor/II.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; ig; 3.
 DR PRINTS; PRO1539; INTERLEUKINR2.
 DR PRINTS; PRO1536; INTRLEUKINR12P.
 DR SMART; SM00409; IG: 3.
 DR Immunoglobulin domain; Receptor; Glycoprotein; Transmembrane; Signal;
 KW Repeat.
 FT SIGNAL 1 13 POTENTIAL.
 FT CHAIN 14 398 INTERLEUKIN-1 RECEPTOR, TYPE II.
 FT DOMAIN 14 343 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 344 369 POTENTIAL.
 FT DOMAIN 370 398 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 43 115 IG-LIKE C2-TYPE DOMAIN 1.
 FT DOMAIN 145 214 IG-LIKE C2-TYPE DOMAIN 2.
 FT DOMAIN 251 333 IG-LIKE C2-TYPE DOMAIN 3.
 FT DISULFID 50 108 BY SIMILARITY.
 FT DISULFID 152 207 BY SIMILARITY.
 FT DISULFID 258 326 BY SIMILARITY.
 FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 219 219 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 123 123 L -> F (IN REF. 2).
 FT CONFLICT 171 171 K -> R (IN REF. 2).
 FT

FT	CONFLICT	199	199	L -> 0 (IN REF. 2).
50	SEQUENCE	398 AA:	45421 MW;	2C2A03ADAEF3AC5B CR664;
	Query Match		6.9%;	Score 252; DB 1; Length 398;
	Best Local Similarity	23.4%;	Pred. No. 1e-11;	
	Matches 79;	Conservative 51;	Mismatches 148;	Indels 60; Gaps 13;
OY	20	ASERCDWDGLMTNRQIQVEDEPARIKCFLHEFLKFNYSIAHSAGLTLIWTTRQDRDL	79	
DB	24	AARSRRFRGRHYKREPRRL-EGEPVALRCPOVPMWASVSPR----	INLTWKKNDARSATV	78
OY	80	--EEDPINFLPKNRISKEDVLMFRITLLNDNGNNTYCMLENTTYSKVAPELVYQKSC	137	
DB	79	PCGE-----ETRMMAQDQALMLPLPALDEDSSTVCTTRMNSYCDKMSIELRVFNEDA	131	
OY	138	FNSPMKL PVHKL YIEY-----GIORITCPNVAGYPPSSVKPPTIYMWGCYKIONFN	188	
DB	132	F-----LP-----FISVPQLITLSTGVS--LVCPDSEIFPRDKTDVIGIYKQSKLLDKDN	180	
OY	189	NVIPRCANLSFLI---ALISNNGNTTCVVTPYBENGTFHLITLTVKVGSPRQNAVPIV	245	
DB	181	EKFLSVRGTHLLVMDVALEDAGYRCVLTFAHEGQGVNITRISIEIRIKKKEERT-PVI	239	
OY	246	HSPNDHVVYERKPGEBLLPCTVYFSEFLMDSRNEVWWTIDGKKPDITITDVTINEISIS	305	
DB	240	ISPLKTI--SASLGSRLTIPCCKVFLGTGTPTPLTTMTMTAN-----DTHIESAYPGG	288	
OY	306	RTEDETRTQI-----LSIKKVTSEDLKRSYVC	332	
DB	289	RYTEGPROEYSNNENYIEVPLIFDPVTEDLHMPKC	326	
RESULT 8				
IRL1_MOUSE				
ID	IRL1_MOUSE	STANDARD;	PRT;	337 AA.
AC	P14719;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Interleukin 1 receptor-like 1 precursor (ST2 protein) (T1 protein)			
DE	(Lymphocyte antigen 84)			
GN	IL1RL1 OR ST2 OR ST2L OR LY84.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OC	NCBI_Taxid=10090;			
KP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/c.			
RC	MEDLINE=90092495; PubMed=2532153;			
RC	Tomlnaga S.;			
RT	"A putative protein of a growth specific cDNA from BALB/c-3T3 cells			
RT	is highly similar to the extracellular portion of mouse interleukin 1			
RT	receptor."			
RL	FEBS Lett. 258:301-304(1989).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RP	STRAIN=C3H/He; TRISUB=Sp1en;			
RC	MEDLINE=91355215; PubMed=1832015;			
RC	Tomlnaga S.I.; Jenkins N.A.; Gilbert D.J.; Copeland N.G.;			
RA	Tetsuka T.;			
RT	"Molecular cloning of the murine ST2 gene. Characterization and			
RT	chromosomal mapping."			
RL	Biochim. Biophys. Acta 1090:1-8(1991).			
RL	[3]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=89345536; PubMed=2527364;			
RC	Klemenz R.; Hoffmann S.; Werenickold A.K.;			
RC	"Serum- and oncoprotein-mediated induction of a gene with sequence			
RT	similarity to the gene encoding carcinoembryonic antigen."			
RL	Proc. Natl. Acad. Sci. U.S.A. 86:5708-5712(1989).			
CC	-I- FUNCTION: POSSIBLY INVOLVED IN REGULATION OF T-LYMPHOCYTE			
CC	ACTION.			

```

CC -I- DEVELOPMENTAL STAGE: GROWTH-SPECIFIC EXPRESSION, G1-PHASE OF
CC CELL CYCLE.
CC -I- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -I- SIMILARITY: STRONG, TO INTERLEUKIN-1 RECEPTORS.
CC -----
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CC -----
DR EMBL; Y07519; CAA6812.1; -
DR EMBL; X60184; CAA42742.1; -
DR EMBL; M24843; AAA40160.1; -
DR PIR; S07054; S07054.
DR MGD; MGI:98427; Ilrl1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGc2; 2.
KW Immunoglobulin domain; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 26
FT CHAIN 27 337
FT DOMAIN 35 100
FT DOMAIN 132 194
FT DOMAIN 233 315
FT DISULFID 42 93
FT DISULFID 139 187
FT DISULFID 240 308
FT CARBOHYD 60 60
FT CARBOHYD 101 101
FT CARBOHYD 107 107
FT CARBOHYD 146 146
FT CARBOHYD 176 176
FT CARBOHYD 194 194
FT CARBOHYD 225 225
FT CARBOHYD 259 259
FT CARBOHYD 278 278
FT VARIAM 192 192
SQ SEQUENCE 337 AA; 38502 MW; 7574372722486926 CRC64.
Query Match 6.3%; Score 230.5; DB 1; Length 337;
Best Local Similarity 23.3%; Pred. No. 3.5e-10;
Matches 90; Conservative 60; Mismatches 135; Indels 101; Gaps 18;
QY 4 LW--CVSLVYTYGIIQSASERCDWGLDTRKIQIOWFDEPARIKPLFEHFLKFNSTIA 61
DB ||:::||||:::||||:::||||:::||||:::||||:::||||:::||||:::
QY 9 LWALILTLTPWY-LTVTEGSK--SSWG-----ENELIYRCP-----ORGRST- 49
QY 62 HSAGLTLVWYTRQORDLEEPINFLPENRISKEDVWMPFPTLINDNTYMLRNTTY 121
DB 50 ----YPMWYTS---DNESIPPTQ-KENRKFVSRDLKFLPARVEDSGIAYCIRSENL 100
QY 122 CSKVAPELEVYQKDSCEPSPMKLPEVHKLYIEYGIOR-----ITCPNWDGYPSSVKPT 174
DB 101 NKTGYLANVTIHKKPSNCIIPD-----YLMYSYVRGSDKNKFKITCPTIDLY--NMTAP 150
QY 175 ITWYMGCKYKION-----FNNVLPESGMISFLIALISNNGNTTCVYTYENGRTF 223
DB 151 VQWFMNCKALQEPFRFARHSYLPIDNVTYHD-----DEGDYTCQPTHAENGNTY 198
QY 224 HLTRLTLTKVWGSPKNANVPYIHSNPNHVVYKESGEELIPCTVYVS-----FLMDSNE 279
DB 199 IYTAIRSFTEVEKSGSMFPVITNPYNITM-EVEIGKPASTACGACGKSGHPLAD---- 253
QY 280 VWMITDGKKPDITIDVYNESISHSRFEDE-----TRTOILSIKYTYSBDLK 327
DB 254 VLM-----QINKTVGNFGGARIQEBEGNNESSNMDCGLTSVLRITGVTEKDLS 303
QY 328 RSYVCHAPSANGEVAKAKVAKOKVPA 353

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DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003600; Ig_like.
 DR InterPro: IPR004078; Interlnk1_BP.
 DR Pfam: PF00047; Ig_3.
 DR PRINTS; PRO1540; INTERLEUKINBP.
 DR PRINTS; PRO1536; INTERLEUKIN12P.
 DR SMART; SM00409; Ig; 2.
 DR SMART; SM00410; Ig like; 1.
 DR Immunoglobulin domain; Glycoprotein; Repeat; Signal.
 KW SIGNAL.
 FT CHAIN 1 18
 FT INTERLEUKIN-1 BINDING PROTEIN.
 FT DOMAIN 1 326
 FT IG-LIKE C2-TYPE DOMAIN 1.
 FT DOMAIN 2 135
 FT IG-LIKE C2-TYPE DOMAIN 2.
 FT DOMAIN 3 235
 FT IG-LIKE C2-TYPE DOMAIN 3.
 FT DISULFID 48
 FT BY SIMILARITY.
 FT DISULFID 143
 FT BY SIMILARITY.
 FT DISULFID 242
 FT BY SIMILARITY.
 FT CARBOHYD 80
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 103
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 113
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 206
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 237
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 326 AA; 36593 MW; 7F03F64600BE390 CRC64;

Query Match 5.2%; Score 189; DB 1; Length 326;
 Best Local Similarity 24.0%; Pred. No. 4.8e-07;
 Matches 80; Conservative 60; Mismatches 156; Indels 38; Gaps 16;

QY 8 VSIFY-GLI0SDASERCDMDGDMTMRQIOVFEDPARIKCPLEHFLKPNYSTAHSAAGL 66
 DB 9 LSIFFSSVQTNAPAECDIKG-QYFASFMELNEPVLPEQI-NLTSSGYNL-----L 61
 QY 67 TLIVWTRORDLEEPINFLPENRISKEDVLMFRPTLNDTGNNTYCMLENTTYSKVA 126
 DB 62 LIMEKRGANDRIIPID-----NGSMMLINPT-QSDSGIYICITINERTYCDMMG 111
 QY 127 FPLEVQKDCSPNPKLPHKLYIEYGIORITCPNVDGPPSVKPTITMYMCYKION 186
 DB 112 LNTIVSVSSNIDLSYF-QYINERSTGBMVCENINAFIASVANDIIV-SGHRIR- 167
 QY 187 FNNVIEPGMNLSPILALISNN-GNYTCVVTYPENGRFHLTRITLVKVGSPNNAVPV 244
 DB 168 -NRKQRTGCIITIEVRKNDAGVYICVLEIYIGKTVNTRIVKLEV--RKLIPT 223
 QY 245 HSPNDHVYKEKEGELLIPCTYFSPFLMDSRN-EYVMTIDGKKPDITITVINESIS 303
 DB 224 MQLPDGIYV--SIGSNLTITACRV--SLRPPTDADVFWMISNGMYEEDDGDGRISVA 278
 QY 304 HSRTEDETR--TQIISIKKVTSEDLKRSVCHA 334
 DB 279 NKIYTTDKRVRITSRKINPVEKD-ATTFTCMA 311

RESULT 11
 VB16 COMPLEX STANDARD; PRT; 326 AA.
 ID VB16 COMPLEX
 AC 004523;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-1 binding protein precursor (Protein B16).
 GN B16R OR B15R.
 OS Cowpox virus (CPV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_Taxid=10243;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Brighton red;
 RA MEDLINE=93008237; PubMed=1339315;
 RA Spriggs M.K., Hruby D.E., Maliszewski C.R., Pickup D.J.,
 RA Sims J.E., Buller R.M.L., Vanslyke J.;

RT Vaccinia and cowpox viruses encode a novel secreted interleukin-1-
 binding protein.";
 RL Cell 71:145-152(1992).
 CC -1- FUNCTION: BINDS INTERLEUKIN-1 AND POSSIBLY INTERLEUKIN-6. COULD
 CC PREVENT THESE CYTOKINES REACHING THEIR NATURAL RECEPTORS. IN
 CC CONSEQUENCE THE INFLAMMATORY RESPONSE WOULD BE DIMINISHED AND
 CC VIRUS REPLICATION ENHANCED.
 CC -1- SUBCELLULAR LOCATION: VIRION, CELL SURFACE OR SECRETORY
 CC GLYCOPROTEIN.
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- SIMILARITY: STRONG, TO INTERLEUKIN-1 RECEPTORS.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL; M95202; AA85776.1; -
 DR InterPro: IPR004074; IL1_receptor/IL1.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003600; Ig like.
 DR InterPro: IPR004078; Interlnk1_BP.
 DR Pfam: PF00047; Ig_3.
 DR PRINTS; PRO1540; INTERLEUKINBP.
 DR PRINTS; PRO1536; INTERLEUKIN12P.
 DR SMART; SM00409; Ig; 2.
 DR SMART; SM00410; Ig like; 1.
 DR Immunoglobulin domain; Glycoprotein; Repeat; Signal; Early protein.
 KW SIGNAL.
 FT CHAIN 1 18
 FT INTERLEUKIN-1 BINDING PROTEIN.
 FT DOMAIN 1 326
 FT IG-LIKE C2-TYPE DOMAIN 1.
 FT DOMAIN 2 135
 FT IG-LIKE C2-TYPE DOMAIN 2.
 FT DOMAIN 3 235
 FT IG-LIKE C2-TYPE DOMAIN 3.
 FT DISULFID 48
 FT BY SIMILARITY.
 FT DISULFID 143
 FT BY SIMILARITY.
 FT DISULFID 242
 FT BY SIMILARITY.
 FT CARBOHYD 80
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 103
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 113
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 237
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 326 AA; 36790 MW; 7AE2064A1FPAF54 CRC64;

Query Match 5.1%; Score 187; DB 1; Length 326;
 Best Local Similarity 25.4%; Pred. No. 6.8e-07;
 Matches 85; Conservative 60; Mismatches 147; Indels 42; Gaps 19;

QY 10 LRYF-GLI0SDASERCDMDGDMTMRQIOVFEDPARIKCPLEHFLKPNYSTAHSAAGL 68
 DB 11 IFFYSSVQAFNAPAECDIKG-QYFASFMELNEPVLPEQI-NLTSSGYNLIL 63
 QY 69 LMYWTRORDLEEPINFLPENRISKEDVLMFRPTLNDTGNNTYCMLENTTYSKVA 128
 DB 64 LIMEKRGANDRIIPID-----NGSMMLINPT-QSDSGIYICITINERTYCDMMG 113
 QY 129 FPLEVQKDCSPNPKLPHKLYIEYGIORITCPNVDGPPSVKPTITMYMCYKION- 186
 DB 114 LTVV--SVGSNIDLSYQIYINERTGBMVCENINAFIASVANDIIV-SGHRIR 169
 QY 187 -FNNVIEPGMNLSPILALISNN-GNYTCVVTYPENGRFHLTRITLVKVGSPNNAVPV 245
 DB 170 RLQRPFPGITIDVVR--NDAGVYICVLEIYIGKTVNTRIVKLEV--RDRMLPTM 224
 QY 246 HSPNDHVYKEKEGELLIPCTYFSPFLMDSRN-EYVMTIDG-KPDITITVINESI 302
 DB 225 QLP-DGVV--TSIGSNLTITACRV--SLRPPTDADVFWMISNGMYEEDDGDGRISVA 278
 QY 303 HSRTEDETR--TQIISIKKVTSEDLKRSVCHA 334
 DB 279 NKIYTTDKRVRITSRKINPVEKD-ATTFTCMA 311

CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Plasma membrane and
 CC phagosomes.
 CC -1- SIMILARITY: BELONGS TO THE TOLL-LIKE RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 TIR DOMAIN.
 CC -1- SIMILARITY: CONTAINS 9 LEUCINE-RICH REPEATS (LRR).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AY009154; AAC37302.1; -;
 DR EMBL: AF316985; AAC35062.1; -;
 DR HSSP: O60603; 1FTW.
 DR MGD: MGI:1341295; TIR1.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_Cterm.
 DR InterPro: IPR003592; LRR_out.
 DR InterPro: IPR003591; LRR_Tyr.
 DR InterPro: IPR00157; TIR_domain.
 DR Pfam: PF00560; LRR; 8.
 DR Pfam: PF01463; LRRCT; 1.
 DR Pfam: PF01582; TIR; 1.
 DR PRINTS: PRO0019; LEURICRPT.
 DR SMART: SM00370; LRR; 3.
 DR SMART: SM00082; LRRCT; 1.
 DR SMART: SM00369; LRR_Tyr; 6.
 DR SMART: SM00255; TIR; 1.
 DR PROSITE: PS50104; TIR; 1.
 DR Receptor; Immune response; Inflammatory response; Signal;
 DR Transmembrane; Repeat; Leucine-rich repeat; Glycoprotein.
 KM TIR SIGNAL 1 25
 FT CHAIN 26 795
 FT DOMAIN 26 582
 FT TRANSMEM 583 603
 FT DOMAIN 604 795
 FT REPEAT 46 70
 FT REPEAT 71 94
 FT REPEAT 96 116
 FT REPEAT 117 140
 FT REPEAT 174 197
 FT REPEAT 200 223
 FT REPEAT 247 270
 FT REPEAT 296 319
 FT REPEAT 333 356
 FT CARBOHYD 432 432
 FT CONFLICT 88
 SQ SEQUENCE 795 AA: 90672 MW: 8553564298720232 CRC64;
 Query Match 4.7%; Score 174; DB 1; Length 795;
 Best Local Similarity 20.2%; Pred. No. 2.3e-05;
 Matches 117; Conservative 95; Mismatches 200; Indels 166; Gaps 26;
 QY 98 VLMPP-----TLNDNTNYTCMLNTTYCSKVAFLPFLVQKDSGFNSPMTLPVHKYI 151
 DB 270 IYWHIPVVKFSSINVTGQQLAFKRMENYSDTSIKALSHQVTD-VFSPQSY-ITSIFA 327
 QY 152 EYGIQRTCPN---VDGYPSSVVKPTI-----TWYGCYKI 184
 DB 328 NNNTIGFTWSTGTHVMVMLCPSSQVSPFLAVDPTDNLITDVMVFKDCRNLVRLKTLISLQKQGL 387

QY 185 QNFNNVPEGNLSPFLIAL-LSNNGNYTCVTPYPPNGRTFHLITLV-----KYVSP 237
 DB 388 KNLNENIILTSAMKTSLOKLDISONS-----LRYSDGIPCAWTSGLVNLSSNMLTGSV 442
 QY 238 KNAVPP-----VIHSPDHVYFEKRGEL-----LIPTVYFSLMDR 277
 DB 443 FRCPLPKVKVLDLHNNRIMSIPKQ--VYHLOALDELAVASNSLTDLPGGARSS----- 494
 QY 278 NEVWMTIDOKKDDITIDVTINESISHRTED-----ETRTQI 315
 DB 495 -----LSVLVIDNSVSHR-SEDFPQSCNIRSLTAGNPPQCTCELRDVR 539
 QY 316 LSIRKVTSEDLK---RSYVC-HARSAKGEVAKAKYKOKPAPRYTVELACFGATVLLV 371
 DB 540 KNIGVAREVAGWPDSTRCDVPSSRGATLADPHMS---PLSCDTVLLTIGATMLVL 596
 QY 372 VI---LIVVHVHVLNVLV-----YRAHGTDETLIDGKEYDIYYSYARNAEEERY 421
 DB 597 AVTGAFLCLYFPLPVYVRLCMQOTRHRARHPILEELQRLNQLFAPVSY--SGHDSAVV 654
 QY 422 LITLGLVENERGYLCLIFDRSLPGNTEVAVPFIQSRBMIVLSPDYVT----- 474
 DB 655 KNEILPNLEKD-DIQICLHERNFVPEKSTVENIINFTEKSYKIFVLSHPFIQSEKCHYE 713
 QY 475 -----EKSISMLPEFKLGVMCONSIATKLIVERYPLEHPHGLIQLKESVSVSM 524
 DB 714 LYFAHNLHFEHSDYLILALPIQYSIPT-----NHKLR-----TMSRRYTLWM 761
 QY 525 KGEKSHSGSKFKWALRLALPLRSLSASSGWNSSCSQ 562
 DB 762 PTEKNKH--GLFWANIRASINVLVNOAGE--TCYTO 794
 RESULT 14
 TLR2 HUMAN STANDARD; PRT; 784 AA.
 AC 060603; 015454;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Toll-like receptor 2 precursor (Toll/interleukin 1 receptor-like protein 4).
 GN TLR2 OR TIL4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leukocyte, and Prostate;
 RX MEDLINE=98261424; PubMed=959645;
 RA Chaudhary P.M., Ferguson C., Nguyen V., Nguyen O., Maesa H.F., Eby M., Jasmin A., Trask B.J., Hood L., Nelson P.S.;
 RT "Cloning and characterization of two Toll/interleukin-1 receptor-like genes TIL3 and TIL4: evidence for a multi-gene receptor family in humans";
 RL Blood 91:4020-4027 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=98118556; PubMed=9435236;
 RT Rock F.L., Hardiman G., Timans J.C., Kastelein R.A., Bazan J.F.;
 RL "A family of human receptors structurally related to Drosophila Toll";
 RN Proc. Natl. Acad. Sci. U.S.A. 95:588-593 (1998).
 RN [3]
 RP SEQUENCE FROM N.A., AND RESPONSE TO LIPOPOLYSACCHARIDE.
 RC TISSUE=Fetal lung;
 RX MEDLINE=98421677; PubMed=9751057;
 RA Yang R.-B., Mark W.R., Gray A., Huang A., Xie M.H., Zhang M., Goddard A., Wood W.I., Gurney A.L., Godowski P.J.;
 RT "Toll-like receptor-2 mediates lipopolysaccharide-induced cellular signaling";
 RL Nature 395:264-268 (1998).

RN [4]
 RP RESPONSE TO BACTERIAL LIPOPROTEINS.
 RX MEDLINE:99357867; PubMed:10426996;
 RA Aliprantis A.O., Yang R.-B., Mark M.R., Suggest S., Devaux B.,
 RA Radolf J.D., Klimek G.R., Godowski P.J., Zychlinsky A.;
 RT "Cell activation and apoptosis by bacterial lipoproteins through
 RT Toll-like receptor-2.";
 RL Science 285:736-739 (1999).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF TIR DOMAIN, AND MUTAGENESIS.
 RX MEDLINE:20531768; PubMed:1081518;
 RA Xu Y., Tao X., Shen B., Horng T., Medzhitov R., Manley J.L., Tong L.;
 RT "Structural basis for signal transduction by the Toll/interleukin-1
 RT receptor domains.";
 RL Nature 408:111-115 (2000).
 CC -I- FUNCTION: Cooperates with MD-2 to mediate the innate immune
 CC response to bacterial lipoproteins and other microbial cell wall
 CC components. Acts via MyD88 and TRAF6, leading to NF-kappa-B
 CC activation, cytokine secretion and the inflammatory response. May
 CC also promote apoptosis in response to lipopeptides. Recognizes
 CC mycoplasma macrophage-activating lipopeptide-2KD (MALP-2),
 CC soluble tuberculous factor (STF), phenol-soluble modulin (PSM)
 CC and B.burgetteri outer surface protein A lipoprotein (OspA-L)
 CC cooperatively with TLR6.
 CC -I- SUBUNIT: Binds MD-2 and TLR6 via the extracellular domain. Binds
 CC MyD88 via their respective TIR domains.
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
 CC -I- TISSUE SPECIFICITY: Highly expressed in peripheral blood
 CC leukocytes, in particular in monocytes, in bone marrow, lymph node
 CC and in spleen. Also detected in lung and in fetal liver. Levels
 CC are low in other tissues.
 CC -I- PTM: N-glycosylated (by similarity).
 CC -I- SIMILARITY: BELONGS TO THE TOLL-LIKE RECEPTOR FAMILY.
 CC -I- SIMILARITY: CONTAINS 1 TIR DOMAIN.
 CC -I- SIMILARITY: CONTAINS 14 LEUCINE-RICH REPEATS (LRR).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF051152; AAC34377.1; -
 CC EMBL: U88878; AAC34133.1; -
 CC Genew: HGNC:11848; TLR2.
 CC MIM: 603028; -
 CC PDB: 1PYW; 22-NOV-00.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_Cterm.
 DR InterPro: IPR003591; LRR_Typ.
 DR InterPro: IPR00157; TIR_domain.
 DR Pfam: PF00560; LRR; 6.
 DR Pfam: PF01463; LRRCT; 1.
 DR Pfam: PF01582; TIR; 1.
 DR SMART: SM00082; LRRCT; 1.
 DR SMART: SM00369; LRR_Typ; 2.
 DR SMART: SM00255; TIR; 1.
 DR PROSITE: PS50104; TIR; 1.
 DR Receptor: Immune response; Inflammatory response; Signal;
 DR Transmembrane; Repeat; Leucine-rich repeat; Glycoprotein;
 DR 3D-structure.
 KW 3D-structure.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 784 TOLL-LIKE RECEPTOR 2.
 FT DOMAIN 19 588 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 589 609 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 610 784
 FT REPEAT 51 74 LRR 1.
 FT REPEAT 75 98 LRR 2.
 FT REPEAT 99 122 LRR 3.
 FT REPEAT 124 147 LRR 4.
 FT REPEAT 148 172 LRR 5.

FT REPEAT 173 196 LRR 6.
 FT REPEAT 221 244 LRR 7.
 FT REPEAT 359 384 LRR 8.
 FT REPEAT 386 411 LRR 9.
 FT REPEAT 412 436 LRR 10.
 FT REPEAT 438 456 LRR 11.
 FT REPEAT 457 476 LRR 12.
 FT REPEAT 477 499 LRR 13.
 FT REPEAT 501 521 LRR 14.
 FT DOMAIN 639 784 TIR.
 FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 139 199 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 414 414 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOTAGEN 681 681 P->F: ABOLISHES THE INTERACTION WITH
 FT MYD88. NO EFFECT ON OLIGOMERIZATION OR
 FT ON THE STRUCTURE OF THE TIR DOMAIN.
 FT D -> B (IN REP. 2).
 FT CONFLICT 726 726
 FT SQ SEQUENCE 784 AA; 89837 MW; 7DBE6B24CF1FAFB8 CRC64;
 Query Match 4.5%; Score 164; DB 1; Length 784;
 Best Local Similarity 21.0%; Pred. No. 0.00013;
 Matches 117; Conservative 88; Mismatches 201; Indels 150; Gaps 30;
 QY 30 DTRROIQVEDEPARIKCPLEHFLKFNYSNAGLTIWYTRQDRDLEPINFRLPE 89
 DB 336 ERKRLTVENSKVFLVPCLSOHLKSLEY-----LDLSE--NLNVEE 375
 QY 90 NRISKEEDVLMFPRPT-----INDNGNYCMLNTYCSKVAFLPEVQKDSK 137
 DB 376 YLKSACEDAM--PSLOTLILQNHLSLEKTEGILLTKNLINID-----ISKNSF 425
 QY 138 FNSP--MKLPVHKLYEYGIQRTCNVDGYPSSVKEPTITWYMGCKYQNFNNVPEGM 195
 DB 426 HSPETCPQEPKRYLNLSTRI--HSVIGCIPTKLE-----ILDVSN--NLNLFSL 474
 QY 196 NLSFLAL--ISNNGNTCVVYPENGRTHRLTLTVKVGSPKNAVPIHSPND--HY 252
 DB 475 NLPOLKELYISRK---LMTLPDASL--LPMILVTK--SRNAITTPSKQOLDSFPH 524
 QY 253 VKEKEGEELLIPCTVYFPEFLMDSRNEVWMTIDGKKPDITITVTN---ESISRTEG 309
 DB 525 LKTLKLGANNFICSEFLF-----TOEQALAVLIDWPANVLCDSHVRGO-- 573
 QY 310 ERTTQLISIKVTSDEPKESVCHANSAGEVAKAKVOKVPAPRYTYELACPGATVU 369
 DB 574 ---QVDVRLSVSE-----CH-----RTLAVS-----GMCCLFLIL 603
 QY 370 LVVILLVVVHVWLVWLVFYRAHFGTDTILDSKE-----YDIYVSYA--RNAEE 417
 DB 604 LIGVLCHRPHGLMYMMWMM-----AMLOAKRRPRAPSNNICYDAVPSSEDAW 654
 QY 418 EEFVLLTLGLVLENEEG--YKLCIFPRDSLPGGNTVEAVDFIORSRMIVVLSPDYVE 475
 DB 655 VENLMVQ---ELEN--FNPFKLCIHRDPIPGKIINDIIDSLSKHKTVFLSEFVVS 710
 QY 476 K---SISMLEFKLVGMCONSIAATKLIY---VEYRPLEHPHPIQLQKESVSFVSKGEK 528
 DB 711 EWCKYELDFSHFRL--FDENNDAAILILEPIEKKAIPORFCIARKIMTKYTLLEWPMDS 768
 QY 529 SKHSKSKPKAKRLAL 544
 DB 769 AOREG--FWVNLDAI 782
 RESULT 15
 ID TLR6_HUMAN STRAND; PRT; 796 AA.
 AC 0912G9;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Toll-like receptor 6 precursor.

GN TLR6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RC MEDLINE=99250250; PubMed=10231569;
RA Takeuchi O., Kawai T., Santo H., Copeland N.G., Gilbert D.J.,
RA Jenkins N.A., Takeda K., Akira S.,
RT "TLR6: A novel member of an expanding Toll-like receptor family.";
RL Gene 231:59-65(1999).
RP FUNCTION.
RX MEDLINE=21334385; PubMed=1141107;
RX Bulut Y., Faure E., Thomas U., Equils O., Arditi M.,
"Cooperation of Toll-like receptor 2 and 6 for cellular activation by
soluble tuberculosis factor and Borrelia burgdorferi outer surface
protein A lipoprotein: role of Toll-interacting protein and Il-1
receptor signaling molecules in Toll-like receptor 2 signaling.";
RL Immunol. 167:987-994(2001).
CC -1- FUNCTION: Participates in the innate immune response to Gram-
positive bacteria and fungi. Acts via MyD88 and IRAK4, leading to
NF-kappa-B activation, cytokine secretion and the inflammatory
response. Recognizes mycoplasma macrophage-activating
lipopeptide-2KD (MALP-2), soluble tuberculosis factor (STF),
phenol-soluble modulin (PSM) and B.burgdorferi outer surface
protein A lipoprotein (OspA-L) cooperatively with TLR2.
CC -1- SUBUNIT: Binds TLR2 via their respective extracellular domains.
CC Binds MyD88 via their respective TIR domains (by similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Plasma membrane and
phagosomes (by similarity).
CC -1- TISSUE SPECIFICITY: Detected in monocytes, CD11c+ immature
dendritic cells, plasmacytoid pre-dendritic cells and dermal
microvessel endothelial cells.
CC -1- SIMILARITY: BELONGS TO THE TOLL-LIKE RECEPTOR FAMILY.
CC -1- SIMILARITY: CONTAINS 1 TIR DOMAIN.
CC -1- SIMILARITY: CONTAINS 13 LEUCINE-RICH REPEATS (LRR).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AB020807; BAA78631.1; -.
DR HSSP; O60603; 1FTW. TLR6.
DR Genew; HGNC:16711; TLR6.
DR MIM; 605403; -.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR003592; LRR_out.
DR InterPro; IPR000157; TIR_domain.
DR Pfam; PF00560; LRR; 6.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PR00019; LEURICRPT.
DR SMART; SM00370; LRR; 2.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS01014; TIR; 1.
DR Receptor; Immune response; Inflammatory response; Signal;
KW Transmembrane; Repeat; Leucine-rich repeat; Glycoprotein.
FT SIGNAL 1 31
FT CHAIN 32 796 TOLL-LIKE RECEPTOR 6.
FT DOMAIN 32 586 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 587 607 POTENTIAL.
FT DOMAIN 608 796 CYTOPLASMIC (POTENTIAL).
FT REPEAT 51 74 LRR 1.
FT REPEAT 75 98 LRR 2.

FT REPEAT 100 120 LRR 3.
FT REPEAT 121 144 LRR 4.
FT REPEAT 158 175 LRR 5.
FT REPEAT 176 201 LRR 6.
FT REPEAT 222 248 LRR 7.
FT REPEAT 276 302 LRR 8.
FT REPEAT 302 328 LRR 9.
FT REPEAT 340 366 LRR 10.
FT REPEAT 366 392 LRR 11.
FT REPEAT 392 418 LRR 12.
FT REPEAT 418 444 LRR 13.
FT DOMAIN 444 784 TIR.
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 214 214 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 253 253 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 359 359 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 423 423 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 434 434 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 583 583 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 796 AA; 91889 MW; 35CEAEC05BFA8BD CRC64;

Query Match 4.5%; Score 163.5; DB 1; Length 796;
Beet Local Similarity 20.3%; Pred. No. 0.00015;
Matches 118; Conservative 91; Mismatches 192; Indels 179; Gaps 26;

QY 103 PTLNDTGN-----YTCMR-----NTTYSKV-----APF 128
DB 249 PTLNFTLNHLETTWKCIWVQPLMPREVLYNIYNTLIESIREDEFTYSKTLKALT 308
QY 129 LEVQKDSQFNSPKMLPHKLYIEYGIQRI-----CPNDGYFSSVK----- 172
DB 309 IHHITNOVFLPSQML--YTFSENNIMTLTSDTPFIHMLCPHA--PSTFKELNFTQ 362
QY 173 --PTTWGTCYKQIONFNVI--PEGNNLSPLIALIS-----NNGNYTC 212
DB 363 NVFTSIEFKSTLYKLETLIQKNGLDLPFGVGMTOMPSLELDVSNLSGSRHKS 422
QY 213 VVTYENGRTFLNRTLVKRVGSPKNAVPPY-----HSPNDHYVKEKPEELLIPCT 267
DB 423 NCTWVESIVLVLSNMM--LTDVFRCLPPRIKYLDSNKKIKSPKQVNVLEMLQELN 479
QY 268 VYFSLMDSRNVMTTIOG--KKPDITDITVINESISHRTE----- 308
DB 480 VAFNSLTD-----LRQGSFSSLSVLIIDHNSVSHPSADPFOSCOQMSIKAGDNPF 531
QY 309 ---DEFTQILSIKKVTSIDLK--RSYVC--HARSAGEVAKAKVKOPAPRYTVELA 361
DB 532 OCTCLAREFVNKIDVSSSEVLGWDSTYKCDYPSYRSPLKDFMS-----ELS 581
QY 362 CG-----FGATVLLVILIVVHYV-----WLEMLVLY-----RAHGTDETLIDGKE 404
DB 582 CNIITLIVTIGATMLVAVTVSLCLIVDLPWYLMVCOQTORRARNIIPLEEQRNQ 641
QY 405 YDIYVSYARNAREEFVLLTLAGVLENFYKLCIFPDDSLPGAGTVAVAPFIOGRBM 464
DB 642 FFAFTSYSEH--DSAMVSELVPIYLEKE--DIQICLHERNPFGKSIVENITINICKSYKS 698
QY 465 IVLSPPDYVT-----EKSIEMLEPKGVKQNCQNSIATGLIYVEYRPLEH 507
DB 699 IVLSPPNFVQSKWCHYEYFAHNLPHGSSNNLILILEPPIQNSIPNK-----YHKLK- 752
QY 508 PRRGILQKESVSPVSKGKSGKSGKSPKALRIALPIR 547
DB 753 -----ALMTQGTVYQMPKESKR--GLFWANIRAAFPNK 784

Search completed: April 23, 2003, 08:52:18
Job time : 32 secs

GenCore version 5.1.4.P5.4578
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OM protein - protein search, using sw model

Run on: April 23, 2003, 08:45:00 ; Search time 95 Seconds

(without alignments)
1490.046 Million cell updates/sec

Title: US-10-061-727-2

Perfect score: 3669
Sequence: 1 MTLWCVSLYFYGIQSDA.....SALALHFTDLSNNDFYLL 687

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2586	70.5	570	4	014915
2	2327.5	63.4	570	11	Q61730
3	2313.5	63.1	570	11	Q63621
4	1892	51.6	356	4	Q9NPH3
5	1663	45.3	360	11	Q8VCB9
6	825	22.5	686	4	Q9NPH6
7	817.5	22.3	658	4	Q9NPH6
8	806.5	22.0	686	11	Q9NPH6
9	769.5	21.0	696	4	Q9NPH6
10	767.5	20.9	696	4	Q9NPH6
11	528	14.4	541	4	Q13478
12	496	13.5	555	13	Q90874
13	479	13.1	537	11	Q61098
14	478	13.0	567	6	Q05208
15	477.5	13.0	573	6	Q9TV71
16	471.5	12.9	599	4	Q95256

17	470	12.8	566	11	Q62611	Q62611 ractus norv
18	466	12.7	574	11	Q9ERS7	Q9ERS7 mus musculu
19	463.5	12.6	556	4	Q9UQ44	Q9UQ44 homo sapien
20	457.5	12.5	533	13	Q9DER5	Q9DER5 gallus galli
21	457.5	12.5	533	13	Q9DER1	Q9DER1 gallus galli
22	457	12.5	561	11	Q62929	Q62929 ractus norv
23	446	12.2	614	11	Q922B1	Q922B1 mus musculu
24	445.5	12.1	575	4	Q9HB29	Q9HB29 homo sapien
25	444.5	12.1	562	4	Q13525	Q13525 homo sapien
26	428.5	11.7	354	11	Q9ER66	Q9ER66 mus musculu
27	390	10.6	486	13	Q9DER4	Q9DER4 gallus galli
28	390	10.6	486	13	Q9DER2	Q9DER2 gallus galli
29	347.5	9.5	571	13	Q8QFN4	Q8QFN4 salmo salar
30	258	7.0	280	11	Q62692	Q62692 ractus norv
31	239.5	6.5	403	6	Q9N2H5	Q9N2H5 equus caball
32	228	6.2	321	13	Q9DER6	Q9DER6 gallus galli
33	228	6.2	321	13	Q9DER3	Q9DER3 gallus galli
34	222.5	6.1	410	4	Q9H733	Q9H733 homo sapien
35	220	6.0	336	11	Q62612	Q62612 ractus norv
36	214	5.8	409	11	Q9JLZ8	Q9JLZ8 mus musculu
37	196.5	5.4	1356	5	Q8WRE2	Q8WRE2 anopheles g
38	192.5	5.2	795	5	Q9NPK8	Q9NPK8 drosophila
39	192.5	5.2	795	5	Q9XZP9	Q9XZP9 drosophila
40	192.5	5.2	795	5	Q9VJX9	Q9VJX9 drosophila
41	190	5.2	326	12	Q8V4R4	Q8V4R4 monkeypox v
42	189.5	5.2	1152	5	Q8WRE5	Q8WRE5 anopheles g
43	189	5.2	326	12	Q57261	Q57261 vaccinia vi
44	189	5.1	5198	5	Q76518	Q76518 caenorhabd
45	188	5.1	441	13	Q9DDC4	Q9DDC4 oncornychnu

ALIGNMENTS

RESULT 1	014915	PRELIMINARY;	PRT;	570 AA.
ID	014915	014915		
AC	014915	PRELIMINARY;	PRT;	570 AA.
DT	01-JAN-1998	(TREMBLrel. 05, Created)		
DT	01-JUN-1998	(TREMBLrel. 05, Last sequence update)		
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)		
DE	IL-1 receptor accessory protein (Membrane interleukin 1 receptor accessory protein).			
GN	IL1RAP.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=PLACENTA;			
RA	Huang J., Gao X., Li S., Cao Z.;			
RL	Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1997).			
RN	(2)			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=BRAIN;			
RA	Saito T., Seki N.;			
RL	Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.			
RN	(3)			
RP	SEQUENCE OF 118-179 FROM N.A.			
RX	MEDLINE=98140136; PubMed=9479509;			
RA	Dale M., Hammond D.W., Cox A., Nicklin M.J.H.;			
RT	"The human gene encoding the interleukin-1 receptor accessory protein (IL1RAP) maps to chromosome 3q28 by fluorescence in situ hybridization and radiation hybrid mapping."			
RL	Genomics 47:325-326(1998).			
RN	(4)			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20261666; PubMed=10799889;			
RA	Jensen L.B., Muzio M., Mantovani A., Whitehead A.S.;			
RT	"IL-1 signaling cascade in liver cells and the involvement of a soluble form of the IL-1 receptor accessory protein."			
RL	J. Immunol. 164:5277-5286(2000).			

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DR EMBL; AF029213; AAB84059.1; -
DR EMBL; AB065537; BAA25421.1; -
DR EMBL; AF016261; AAC39609.1; -
DR EMBL; AF167342; AAF71689.1; -
DR EMBL; AF167335; AAF71689.1; JOINED.
DR EMBL; AF167336; AAF71689.1; JOINED.
DR EMBL; AF167337; AAF71689.1; JOINED.
DR EMBL; AF167338; AAF71689.1; JOINED.
DR EMBL; AF167339; AAF71689.1; JOINED.
DR EMBL; AF167340; AAF71689.1; JOINED.
DR EMBL; AF167341; AAF71689.1; JOINED.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR004075; IL1_receptor1.
DR InterPro; IPR000157; TIR_domain.
DR Pfam; PF00047; IG_2.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PRO1537; INTRLNRI1F.
DR SMART; SM00409; IG; 2.
DR SMART; SM00255; TIR; 1.
KW Receptor.
SQ SEQUENCE 570 AA; 65418 MW; 5F478D0ECA98B8A CRC64;

Query Match 70.5%; Score 2586; DB 4; Length 570;
Best Local Similarity 85.3%; Pred. No. 5.8e-211;
Matches 488; Conservative 35; Mismatches 37; Indels 12; Gaps 4;

QY 1 MTLIMCVSLYFYGILOSASERCDDWGLDMROIQVFEDEPARIKCPLFEHFLKFNYST 60
DB 1 MTLIMCVSLYFYGILOSASERCDDWGLDMROIQVFEDEPARIKCPLFEHFLKFNYST 60
QY 61 AHSAGLTLLIWMYTRQDRDLPEPINFRLPENRISKEKDVLMFRPTLNDGTGNTCLNNTT 120
DB 61 AHSAGLTLLIWMYTRQDRDLPEPINFRLPENRISKEKDVLMFRPTLNDGTGNTCLNNTT 120
QY 121 YCSVAPELEVVOKDSCEPNSPMKLPVHKLYIEYGIORTCPNDGYPSSVKPTITWYMG 180
DB 121 YCSVAPELEVVOKDSCEPNSPMKLPVHKLYIEYGIORTCPNDGYPSSVKPTITWYMG 180
QY 121 YCSVAPELEVVOKDSCEPNSPMKLPVHKLYIEYGIORTCPNDGYPSSVKPTITWYMG 180
DB 121 YCSVAPELEVVOKDSCEPNSPMKLPVHKLYIEYGIORTCPNDGYPSSVKPTITWYMG 180
QY 181 CYKIQNFNNVPIPEGNNLSFLIALISNNNGNTCVVTPYENGRTFHLTRTLTVKVVGPSRNA 240
DB 181 CYKIQNFNNVPIPEGNNLSFLIALISNNNGNTCVVTPYENGRTFHLTRTLTVKVVGPSRNA 240
QY 241 VPPVISHPNDHVYKEKEGEELIPCTVYFSFLMDSRNEVWMTIDGKKPDITIDVTINE 300
DB 241 VPPVISHPNDHVYKEKEGEELIPCTVYFSFLMDSRNEVWMTIDGKKPDITIDVTINE 300
QY 301 SISHSRTEDETRTOILSIKVTSEDLKRSYVCHARSAKGEVAKAKVOKVAPRYTVEL 360
DB 301 SISHSRTEDETRTOILSIKVTSEDLKRSYVCHARSAKGEVAKAKVOKVAPRYTVEL 360
QY 301 SISHSRTEDETRTOILSIKVTSEDLKRSYVCHARSAKGEVAKAKVOKVAPRYTVEL 360
DB 301 SISHSRTEDETRTOILSIKVTSEDLKRSYVCHARSAKGEVAKAKVOKVAPRYTVEL 360
QY 361 ACFGATVLLVLLIVVHYVWLEMLFYRAHFGTDETLIDGKEYDIYVSARNAEEEF 420
DB 361 ACFGATVLLVLLIVVHYVWLEMLFYRAHFGTDETLIDGKEYDIYVSARNAEEEF 420
QY 421 VLLTRGVLENEFGYKLCIFDRDSLPGNTVEAVDFIQSRMIVVLSPPDYTESKISM 480
DB 421 VLLTRGVLENEFGYKLCIFDRDSLPGNTVEAVDFIQSRMIVVLSPPDYTESKISM 480
QY 481 LEFLGVMCNSIATK----LIVVEYRPLEBHPHPIGLQKES--VSFVSMKEKSKHSG 533
DB 481 LEFLGVMCNSIATK----LIVVEYRPLEBHPHPIGLQKES--VSFVSMKEKSKHSG 533
QY 481 LEFLGVMCNSIATK----LIVVEYRPLEBHPHPIGLQKES--VSFVSMKEKSKHSG 533
DB 481 LEFLGVMCNSIATK----LIVVEYRPLEBHPHPIGLQKES--VSFVSMKEKSKHSG 533
QY 534 SKFWKALRLALPLRSLASAGNESCSSOSDI 565
DB 534 SKFWKALRLALPLRSLASAGNESCSSOSDI 565
QY 536 GFWKQLQVAMPVKK--SPRSSSDEQGLSYSSL 567
DB 536 GFWKQLQVAMPVKK--SPRSSSDEQGLSYSSL 567

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DT 01-NOV-1996 (Tremblrel. 01, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DR Interleukin 1 receptor accessory protein precursor.
GN IL1RAP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid:10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95293970; PubMed=775431;
RA Gelfand S.A., Nunez P., Kwee L., Labow M., Chizzonite R.A., Ju G.;
RT Molecular cloning and characterization of a second subunit of the
RT Interleukin 1 receptor complex.
RT J. Biol. Chem. 270:13757-13765 (1995).
DR EMBL; X85999; CAA59991.1; -.
DR MGI; MGI:104975; Il1rap.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR004075; IL1_receptor1.
DR InterPro; IPR000157; TIR_domain.
DR Pfam; PF00047; IG; 3.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PRO1537; INTRLNRI1F.
DR SMART; SM00409; IG; 2.
DR SMART; SM00255; TIR; 1.
KW Receptor; Signal.
FT SIGNAL 1 20
SQ SEQUENCE 570 AA; 65740 MW; 4D4B07E0310AFDC5 CRC64;

Query Match 63.4%; Score 2327.5; DB 11; Length 570;
Best Local Similarity 75.9%; Pred. No. 5.3e-189;
Matches 429; Conservative 66; Mismatches 55; Indels 15; Gaps 5;

QY 1 MTLIMCVSLYFYGILOSASERCDDWGLDMROIQVFEDEPARIKCPLFEHFLKFNYST 60
DB 1 MGLIMVLSLSTFYGILOSASERCDDWGLDMROIQVFEDEPARIKCPLFEHFLKFNYST 60
QY 61 AHSAGLTLLIWMYTRQDRDLPEPINFRLPENRISKEKDVLMFRPTLNDGTGNTCLNNTT 120
DB 61 AHSAGLTLLIWMYTRQDRDLPEPINFRLPENRISKEKDVLMFRPTLNDGTGNTCLNNTT 120
QY 121 YCSVAPELEVVOKDSCEPNSPMKLPVHKLYIEYGIORTCPNDGYPSSVKPTITWYMG 180
DB 121 YCSVAPELEVVOKDSCEPNSPMKLPVHKLYIEYGIORTCPNDGYPSSVKPTITWYMG 180
QY 121 YCSVAPELEVVOKDSCEPNSPMKLPVHKLYIEYGIORTCPNDGYPSSVKPTITWYMG 180
DB 121 YCSVAPELEVVOKDSCEPNSPMKLPVHKLYIEYGIORTCPNDGYPSSVKPTITWYMG 180
QY 181 CYKIQNFNNVPIPEGNNLSFLIALISNNNGNTCVVTPYENGRTFHLTRTLTVKVVGPSRNA 240
DB 181 CYKIQNFNNVPIPEGNNLSFLIALISNNNGNTCVVTPYENGRTFHLTRTLTVKVVGPSRNA 240
QY 241 VPPVISHPNDHVYKEKEGEELIPCTVYFSFLMDSRNEVWMTIDGKKPDITIDVTINE 300
DB 241 VPPVISHPNDHVYKEKEGEELIPCTVYFSFLMDSRNEVWMTIDGKKPDITIDVTINE 300
QY 301 SISHSRTEDETRTOILSIKVTSEDLKRSYVCHARSAKGEVAKAKVOKVAPRYTVEL 360
DB 301 SISHSRTEDETRTOILSIKVTSEDLKRSYVCHARSAKGEVAKAKVOKVAPRYTVEL 360
QY 301 SISHSRTEDETRTOILSIKVTSEDLKRSYVCHARSAKGEVAKAKVOKVAPRYTVEL 360
DB 301 SISHSRTEDETRTOILSIKVTSEDLKRSYVCHARSAKGEVAKAKVOKVAPRYTVEL 360
QY 361 ACFGATVLLVLLIVVHYVWLEMLFYRAHFGTDETLIDGKEYDIYVSARNAEEEF 420
DB 361 ACFGATVLLVLLIVVHYVWLEMLFYRAHFGTDETLIDGKEYDIYVSARNAEEEF 420
QY 421 VLLTRGVLENEFGYKLCIFDRDSLPGNTVEAVDFIQSRMIVVLSPPDYTESKISM 480
DB 421 VLLTRGVLENEFGYKLCIFDRDSLPGNTVEAVDFIQSRMIVVLSPPDYTESKISM 480
QY 481 LEFLGVMCNSIATK----LIVVEYRPLEBHPHPIGLQKES--VSFVSMKEKSKHSG 533
DB 481 LEFLGVMCNSIATK----LIVVEYRPLEBHPHPIGLQKES--VSFVSMKEKSKHSG 533
QY 481 LEFLGVMCNSIATK----LIVVEYRPLEBHPHPIGLQKES--VSFVSMKEKSKHSG 533
DB 481 LEFLGVMCNSIATK----LIVVEYRPLEBHPHPIGLQKES--VSFVSMKEKSKHSG 533
QY 534 SKFWKALRLALPLRSLASAGNES 558
DB 534 SKFWKALRLALPLRSLASAGNES 558
QY 536 GFWKQLQVAMPVKK--SPRSSSDEQGLSYSSL 557
DB 536 GFWKQLQVAMPVKK--SPRSSSDEQGLSYSSL 557

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RESULT 3
ID 063621 PRELIMINARY; PRT; 570 AA.
AC 063621;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, last annotation update)
DE Interleukin-1 receptor accessory protein.
IL-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RM [1]
P SEQUENCE FROM N.A.
MEDLINE=96265355; Pubmed=8964912;
Liu C., Chalmers D., Maki R., De Souza E.B.;
"Rat homolog of mouse interleukin-1 receptor accessory protein:
cloning, localization and modulation studies."
J. Neuroimmunol. 66:41-48(1996).
DR EMBL, U48592; AAB03502.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR004075; IL1_receptor1.
DR InterPro: IPR00157; TIR_domain.
DR Pfam: PF00047; Ig_3.
DR Pfam: PF01582; TIR; 1.
DR PRINTS: PR01537; INTERLKN1RLF.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00255; TIR; 1.
KM Receptor.
SQ SEQUENCE 570 AA; 65598 MW; 20C3A5478127AABE CRC64;

Query Match 63.1%; Score 2313.5; DB 11; Length 570;
Best Local Similarity 75.7%; Pred. No. 8.2e-188;
Matches 430; Conservative 62; Mismatches 55; Indels 21; Gaps 5;

QY 1 MTLWCVSILYFYGIQSDASERCDWGLDTWQIOVFEDPARIKCPLFEHFLKKNYST 60
DB 1 MGLPWCMLSLFCGILQSHASERCDWGLDTWQIOVFEDPARIKCPLFEHFLKKNYST 60
QY 61 AHSAGLTILWYTRORDLEEPINFLPENRISKEKDVLMFRPTLLNDTNGNTCMLRNTT 120
DB 61 AHSAGLTILWYTRORDLEEPINFLPENRISKEKDVLMFRPTLLNDTNGNTCMLRNTT 120
QY 121 YCSKVAFLPEVVQKSCFNSPKMLPVHKLXIEXGIQRTCPNVGYPSPSVKPTITWYG 180
DB 121 YCSKVAFLPEVVQKSCFNSPKMLPVHKLXIEXGIQRTCPNVGYPSPSVKPTITWYG 180
QY 181 CYKIQNFNNVPEGMNLSFLIALISNNGNTCVVTPENGRTFHLTRTLTVKVGSPKNA 240
DB 181 CYKIQNFNNVPEGMNLSFLIALISNNGNTCVVTPENGRTFHLTRTLTVKVGSPKNA 240
QY 241 VPPVHISPDHVVYEKEPEBELLIPCTVYPSFLMDSRNEVWMTTIDGKKDDITIDVTINE 300
DB 241 VPPVHISPDHVVYEKEPEBELLIPCTVYPSFLMDSRNEVWMTTIDGKKDDITIDVTINE 300
QY 301 SISHSRTEDETRTQILSIKVTSEDLKRSYVCHARSAGKEVAKAAKVKQVAPRYTEL 360
DB 301 SISHSRTEDETRTQILSIKVTSEDLKRSYVCHARSAGKEVAKAAKVKQVAPRYTEL 360
QY 361 ACQFGATVLLVYLIVYHYVLEMLFPAHAGTDETTIDGKEXYDIYVSARNAEEBF 420
DB 361 ACQFGATVLLVYLIVYHYVLEMLFPAHAGTDETTIDGKEXYDIYVSARNAEEBF 420
QY 421 VLLTLAGVENERGYKCLFDRSLPGQNTVEAVPDFIORBRMIVLSDDYVTEKSI 480
DB 421 VLLTLAGVENERGYKCLFDRSLPGQNTVEAVPDFIORBRMIVLSDDYVTEKSI 480
QY 481 LBEKGLGVNCONSIAIK-----LIVERYRPLEHPHGLQLKE-----SVFVSKGEKSK 530
DB 481 LBEKGLGVNCONSIAIK-----LIVERYRPLEHPHGLQLKE-----SVFVSKGEKSK 530

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DB 481 LBEKGLGVNCONSIAIK-----LIVERYRPLEHPHGLQLKE-----LKVKELRKAKSVLTIVKMGESK 532
QY 531 HSGSKFPMKALRLALPLRSLASAGWNES 558
DB 533 YPGRFWKOLQVAMPYK-----SPRWSS 557

RESULT 4
ID 09NPH3 PRELIMINARY; PRT; 356 AA.
AC 09NPH3;
DT 01-OCT-2000 (TRENBLREL. 15, Created)
DT 01-OCT-2000 (TRENBLREL. 15, last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, last annotation update)
DE Soluble interleukin 1 receptor accessory protein (Soluble interleukin-1 receptor accessory protein).
IL1RAP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RM [1]
P SEQUENCE FROM N.A.
MEDLINE=20261666; Pubmed=10799889;
Jensen L.E., Muzio M., Mantovani A., Whitehead A.S.;
"IL-1 signaling cascade in liver cells and the involvement of a
soluble form of the IL-1 receptor accessory protein."
J. Immunol. 164:5277-5286(2000).
DR EMBL, AF167340; AAF71688.1; -.
DR EMBL, AF167335; AAF71688.1; JOINED.
DR EMBL, AF167336; AAF71688.1; JOINED.
DR EMBL, AF167337; AAF71688.1; JOINED.
DR EMBL, AF167338; AAF71688.1; JOINED.
DR EMBL, AF167339; AAF71688.1; JOINED.
DR EMBL, AF167343; AAF71687.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 2.
DR SMART; SM00409; Ig; 2.
KM Receptor.
SQ SEQUENCE 356 AA; 41019 MW; 39B72452C458A1C3 CRC64;

Query Match 51.6%; Score 1892; DB 4; Length 356;
Best Local Similarity 100.0%; Pred. No. 2.7e-152;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLWCVSILYFYGIQSDASERCDWGLDTWQIOVFEDPARIKCPLFEHFLKKNYST 60
DB 1 MTLWCVSILYFYGIQSDASERCDWGLDTWQIOVFEDPARIKCPLFEHFLKKNYST 60
QY 61 AHSAGLTILWYTRORDLEEPINFLPENRISKEKDVLMFRPTLLNDTNGNTCMLRNTT 120
DB 61 AHSAGLTILWYTRORDLEEPINFLPENRISKEKDVLMFRPTLLNDTNGNTCMLRNTT 120
QY 121 YCSKVAFLPEVVQKSCFNSPKMLPVHKLXIEXGIQRTCPNVGYPSPSVKPTITWYG 180
DB 121 YCSKVAFLPEVVQKSCFNSPKMLPVHKLXIEXGIQRTCPNVGYPSPSVKPTITWYG 180
QY 181 CYKIQNFNNVPEGMNLSFLIALISNNGNTCVVTPENGRTFHLTRTLTVKVGSPKNA 240
DB 181 CYKIQNFNNVPEGMNLSFLIALISNNGNTCVVTPENGRTFHLTRTLTVKVGSPKNA 240
QY 241 VPPVHISPDHVVYEKEPEBELLIPCTVYPSFLMDSRNEVWMTTIDGKKDDITIDVTINE 300
DB 241 VPPVHISPDHVVYEKEPEBELLIPCTVYPSFLMDSRNEVWMTTIDGKKDDITIDVTINE 300
QY 301 SISHSRTEDETRTQILSIKVTSEDLKRSYVCHARSAGKEVAKAAKVKQ 350
DB 301 SISHSRTEDETRTQILSIKVTSEDLKRSYVCHARSAGKEVAKAAKVKQ 350

RESULT 5
ID 08VCB9

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ID 08VCB9 PRELIMINARY; PRT; 360 AA.
AC 08VCB9;
DT 01-MAR-2002 (Tremblere1.20, Created)
DT 01-MAR-2002 (Tremblere1.20, Last sequence update)
DT 01-JUN-2002 (Tremblere1.21, Last annotation update)
DE Similar to interleukin 1 receptor accessory protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC021159; AAI21159.1; -
DR InterPro; IPR003599; IG.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_3.
DR SMART; SM00409; IG_3.
KM Receptor.
SQ SEQUENCE 360 AA; 41567 MW; B525471759FF7719 CRC64;
Query Match 45.3%; Score 1663; DB 11; Length 360;
Best Local Similarity 85.1%; Pred. No. 7, 66-133;
Matches 298; Conservative 30; Mismatches 22; Indels 0; Gaps 0;
QY 1 MTLIMCVSLFYGILOSADSEKCDMDGLDTRQIQVFEDEPARIKCPLEHFLKFNYS 60
DB 1 MGLIMYLSLSPFYGILOSASERCDMDGLDTRQIQVFEDEPARIKCPLEHFLKFNYS 60
QY 61 AHSAGLTIWYTRORDLEEPINRLPENRISKEDVLMFRPTLNDTGNVTCMLRNT 120
DB 61 AHSAGLTIWYTRORDLEEPINRLPENRISKEDVLMFRPTLNDTGNVTCMLRNT 120
QY 121 YCSVAFLPELVQKSCFNSPMKLVHKLIEYGIQRTCPNVNGYFPSSVKPTITWYG 180
DB 121 YCSVAFLPELVQKSCFNSPMKLVHKLIEYGIQRTCPNVNGYFPSSVKPTITWYG 180
QY 121 YCSVAFLPELVQKSCFNSPMKLVHKLIEYGIQRTCPNVNGYFPSSVKPTITWYG 180
DB 121 YCSVAFLPELVQKSCFNSPMKLVHKLIEYGIQRTCPNVNGYFPSSVKPTITWYG 180
QY 181 CYKIQNFNNVPIEGMNLSPILALISNNNGYTCVVTYPENGRFTLRTLVKVGSPRNA 240
DB 181 CYKIQNFNNVPIEGMNLSPILALISNNNGYTCVVTYPENGRFTLRTLVKVGSPRNA 240
QY 241 VPIPIHSPNVHYEKEGEEELIPCTVYPSFLMDSRNEVWMTIDGKKPDITIDVTINE 300
DB 241 LPIPIYSPNDVHYEKEGEEELIPCTVYPSFLMDSRNEVWMTIDGKKPDITIDVTINE 300
QY 301 SISHRTEDTRTQILSIKVTSEDLKRSYVCHARSAKGEVAKAAKVKOK 350
DB 301 SVSSTSEDETRTQILSIKVTSEDLKRSYVCHARSAKGEVAKAAKVKOK 350

RA Sana T.R., Debets R., Timans J.C., Bazan J.F., Kastelein R.A.;
RT "Computational identification, cloning and characterization of IL-1R9,
RT a novel interleukin-1 receptor (IL-1R)-like gene encoded on human
RT chromosome Xq 22.2-22.3";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Grabowski M., Lorenz B., Hubel R., Strom T.M.;
RL "A gene (IL1RAPL-2) with 61% identity to IL1RAPL maps to Xq22.2";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=20459050; PubMed=10882729;
RA Born T.L., Smith D.E., Garika K.E., Renshaw B.R., Bertles J.S.,
RA Sims J.E.;
RT "Identification and characterization of two members of a novel class
RT of the interleukin-1 receptor (IL-1R) family. Delineation of a new
RT class of IL-1R-related proteins based on signaling";
RL J. Biol. Chem. 275:29946-29954(2000).
DR EMBL; AJ290436; CAB89867.1; -
DR EMBL; AF212016; AAF61307.1; -
DR EMBL; AF212208; CAB86868.1; -
DR EMBL; AF284436; CAB21370.1; -
DR InterPro; IPR003599; IG_1;
DR InterPro; IPR003600; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR004075; IL1_receptor1.
DR InterPro; IPR00157; TIR_domain.
DR Pfam; PF00047; IG_3.
DR Pfam; PF01582; TIR_1.
DR PRINTS; PR01537; INTRLNRI1P.
DR SMART; SM00409; IG_2.
DR SMART; SM00410; IG_1like; 1.
DR SMART; SM00255; TIR; 1.
KM Receptor.
SQ SEQUENCE 686 AA; 78669 MW; E400F7ECD16697C CRC64;
Query Match 22.5%; Score 825; DB 4; Length 686;
Best Local Similarity 31.9%; Pred. No. 2, 9e-61;
Matches 228; Conservative 106; Mismatches 244; Indels 136; Gaps 27;
QY 1 MTLIMCVSLFYGILOSADSEKCDMDGLDTRQIQVFEDEPARIKCPLEHFLKFNYS 59
DB 7 LALVACSVSNLKMVSKRNSVDCIDMSVD-LKTVALAGEPRVCAALFYSTRNYS 65
QY 60 TAHSAGLTIWYTRORDLEEPINRLPENRISKEDVLMFRPTLNDTGNVTCMLRNT 119
DB 66 TAQSTGLRIMY--KNGGDLEPIIF--SEVRMKEKEDSIWFHSAEADSGFYTCLRNS 121
QY 120 YCSVAFLPELVQKSCFNSPMKLVHKLIEYGIQRTCPNVNGYFPSSVKP 173
DB 122 TYCMKVSMSLVAENESGLCYNSRIR-----YLEKESEVTKRKEISCPMDDFKKSQEP 175
QY 174 TITWYMGCYKIQNFNNVPIEGMNLSPILALISNNNGYTCVVTYPENGRFTLRTLVK 233
DB 176 DVVWYKECKEPRMRSIIIIQGNALLIOEVBEGDGNVTCLEKT--EGSL--VRRITTEKV 231
QY 234 VGSFKNVAVP-VPIHSPNVHYEKEGEEELIPCTVYPSFLMDSRNEVWMTIDGKKPD 292
DB 232 TALITDPRPPLPFMEQOPVIVDQKPLNIPCKAFFGSGEGPMIYW-MNGEK----- 286
QY 293 TIDVTINESISHRTEDTR-----TQILSIKVTSEDLKRSYVCHARSAKGEV 341
DB 287 ----FIEELAGHIR-EGEIRILKHELKEKEVEALILPDSVEADL--ANYCHVENRGR- 339
QY 342 AKAAKQKVPAPRYTVELACGFGATVLVILIVVHVWVLEWVLYRAHFGDEITLD 401
DB 340 -KASVLLRKQDLIKYKIELAGGLAFILVLVILVYIKYCNITELMFLYRQHPGADBNDD 398
QY 402 GKEYDIIVSYAR-----NAEEEFVLLTLRGVLENEGYGLCFDRDSLPFGANTVE 452
DB 399 NKEVDATLSTKVQDPTLDCDNPPEEQFALVLPDVLEKHYGYLFLPBDLIPSGTYME 458

QY 453 AVDFPQRSRMIVLSPDYTEKRSIMLEPKLGVMCONSIAI---KLIVERYPLEHPH 509
 Db 459 DLFYVQSRRLIVLPDYLRGWSI--FELESRLHMLVSGEIKVILIECTELK--- 513
 QY 510 PG-----ILQKESV---SFSWKGEKSKHSGKFWKALPLR----- 547
 Db 514 -GKVCQEVESIKSLIKLILKMGKSSKLNKSPFWKHLVYEMPIKKEMLPRCHVLD 572
 QY 548 -----SLSSSGNESCSSOSDLSLHVQRRLKEPEPELOS----- 586
 Db 573 AEOGLFGELOPIPSIAIMTSATLVSQADL-----PEFHSDSMQIRHC 617
 QY 587 -----BRAAGSPAPGKMSKGRKSSATCRCCVYCEGNHLRN--KSRAEIH 632
 Db 618 CRGYKHEIPATLPLVPPLSGNH-----TYCNLPITLNGQLPLANNYLKDOEFH 666

JLT 7

Q9NZNO PRELIMINARY; PRT; 658 AA.
 AC Q9NZNO;
 DT 01-OCT-2000 (TEMBLrel. 15, Created)
 DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
 DE X-linked interleukin-1 receptor accessory protein-like 2
 DE (Fragment).
 GN IL1RAPL2.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20218565; PubMed=10757639;
 RA Jin H., Visesvarajah R., Gardner R.J., Roberts R.G.;
 RT "Two novel members of the interleukin-1 receptor gene family, one
 RT deleted in Xp21.3-Xp21.3 mental retardation";
 RL Eur. J. Hum. Genet. 8:87-94(2000).
 DR EMBL; AF181285; AAF59412.1; .
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR003600; IG_1like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR000157; TIR_domain.
 DR Pfam; PF00047; IG_3.
 DR Pfam; PF01582; TIR; 1.
 DR SMART; SM00409; IG_2.
 DR SMART; SM00410; IG_1like; 1.
 DR SMART; SM00255; TIR; 1.
 KM Receptor.
 FT NON_FER 1
 SQ SEQUENCE 658 AA; 75626 MW; 5B7506AF110B12 CRC64;

Query Match 22.3%; Score 817.5; DB 4; Length 658;
 Best Local Similarity 32.3%; Pred. No. 1,2e-60;
 Matches 223; Conservative 99; Mismatches 233; Indels 135; Gaps 26;

QY 24 CDDMGIDTMRQIOVFEDEPARIKCPLEHFLKENVSTRAHSGTLIWMYTRQDDLEBPI 83
 Db 3 CIDMSVD-LKTYMALAGEPVKCALFYSYIRTVSTAGTGLRLMY--KNKGDLEBPI 59
 QY 84 NPLPERRISKEKQVLMFPRPTLNDTGNNTCMANTYCSVAPPLVAVQDS--CNSP 141
 Db 60 IF--SEVMSSEEDSIFWFSAEADDSGYTTLVNSTYCMKSNSTVVAENBSGLCYNSR 117
 QY 142 MKLPVHLTYIEYG---IORITCPNVQDYPSPSVKPTITTYMGCYKIQNFNNVPEGNTL 197
 Db 118 IR-----YLEKSEVTKRKEISCPDMDPKSDDEPDVWYKCKPKKMSITIQKGNAL 171
 QY 198 SFLLALISNNGNNTCVVTPYENGRTFHLTRLTYKVGSPNAAV-PYHSPPNDHVVYK 256
 Db 172 LIGVGEDEGNGNYTCELCY--EGKL--VRRTEELKVTALLTDKPKPLFPWENQPSVIDV 227

QY 257 EPGELLIPCTVYFSLMDSRNEVMWTIDGKPPDITIDVTINESISHSRTEDETR---- 312
 Db 228 QLGKPLNIPCKAPFGFCGSGSPMITY--MKGEK-----FIELAGHIR-EGEIRLLKE 277
 QY 313 -----TQLSTIKVTSSEDLKSYVCHASAKGEVAKAKVQKVPAPRTVYLACFG 365
 Db 278 HLGKEVELLIPDSVVEADL--NAYTCHVENRNR--KHASVLLRKDOLYIKIELAGLG 334
 QY 366 ATVLAVVILIVVHVWLEWLFYRAHGTDETLIDGKEYDIYSVAR-----NAE 416
 Db 335 AIFLLVAVVITKVCYVIELMFLFRQHFGADETNDNKSDAYSTYKVDDPTLDCDNP 394
 QY 417 EEEFVLLTLRGVLENERGYKLCIFDRDSLPGNTVEAVDFPQRSRMIVLSPDYTEK 476
 Db 395 EEOGPALEVLDPVLEKHGYKLFIPERDLIPSGTMEDELTRVVEGSRRLIIVLPDYLR 454
 QY 477 SISMLERKLGVMCONSIAI---KLIVERYPLEHPHQ-----ILQKESV---SFSW 524
 Db 455 GWSI--FELESRLHMLVSGEIKVILIECTELK-----GKVCQEVESIKSLIKL 508
 QY 525 KGEKSKHSGKFWKALPLR-----SLSSSGNNS 558
 Db 509 KGSKSSKLNKSPFWKHLVYEMPIKKEMLPRCHVLDABOGLFGELOPIPSIAIMTSATL 568
 QY 559 CSSQSDISLHVQRRLKEPEPELOS-----BRAAGSPAPGKMSKGRG 604
 Db 569 VSSQADL-----PEFHSDSMQIRHCRCGYGHEIPATLPLVPPLSGNH-- 611
 QY 605 KKSATCRCCVYCEGNHLRN--KSRAEIH 632
 Db 612 ---TYCNLPITLNGQLPLANNYLKDOEFH 638

RESULT 8

Q9ERS6 PRELIMINARY; PRT; 686 AA.
 AC Q9ERS6;
 DT 01-MAR-2001 (TEMBLrel. 16, Created)
 DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
 DE TIGIR-1.
 GN IL1RAPL2.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20459050; PubMed=10882729;
 RA Born T.L., Smith D.E., Garika K.E., Renshaw B.R., Bertles J.S.,
 RA Sims J.E.;
 RT "Identification and characterization of two members of a novel class
 RT of the interleukin-1 receptor (IL-1R) family. Delineation of a new
 RT class of IL-1R-related proteins based on signaling";
 RL J. Biol. Chem. 275:29946-29954(2000).
 DR EMBL; AF284437; AAG21371.1; .
 DR MGD; MGI:1913106; IL1rapl2.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR003600; IG_1like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR000157; TIR_domain.
 DR Pfam; PF00047; IG_3.
 DR Pfam; PF01582; TIR; 1.
 DR SMART; SM00409; IG_2.
 DR SMART; SM00410; IG_1like; 2.
 DR SMART; SM00255; TIR; 1.
 SQ SEQUENCE 686 AA; 78797 MW; 36160D1CDB9B8264 CRC64;

Query Match 22.0%; Score 806.5; DB 11; Length 686;
 Best Local Similarity 32.5%; Pred. No. 1.1e-59;
 Matches 215; Conservative 107; Mismatches 255; Indels 85; Gaps 24;

QY 1 MTLIMC-VVSLYFYGILQSDASERCDMGIDTMRQIOVFEDEPARIKCPLEHFLKFNYS 59

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Db 7 LALVCSAATSTLKWVSKNSVDGCTDMSVD-LKTMALAGEVVRKCLFYIITNTS 65
Qy 60 THASGLTITWTRDRLDLEEPINRLPENRISKEDVLMFRPTLLDNTGNTCLMRT 119
Db 66 MASTGLRLMWY--RNKGLLEPIIF--SEVRMSKEEDAIMFASAEQDSGFYTCVLRS 121
Qy 120 TCSVAAPLEVVOKDS--CFNSPMLPVHKYIEYG---LQICPNVDGFPSVYK 173
Db 122 TCMKVSLSLTVAKENSGCTNSRIR-----YLEKSEVTKREISCDDDDPKKDQEV 175
Qy 174 TITWMCYKIQNFNNVIEGNNLSFLIALISNNGNYTCVVYTPENGRTFHLTRTLTKV 233
Db 176 DVVWYKECKPKMWRSLIIQGNALLIQEVEHGGNYTCELK--BGKL--VARTELKY 231
Qy 234 VSPKQANP-PVHSNDHNVYKEKEGELLIPCTVYPSFLMSDNEVWMTIDGKPPDI 292
Db 232 TALLTDKPKPLPPEMNOPIVDVQKPLNTPCKAFPGSGSGPMIYW-MKGEK--- 286
Qy 293 TIDVTINESISHRTEDTR-----TQIISIKKVTSEDLKRSYVCHARSAGV 341
Db 287 ----FIEELAGHIR-EGELRLKELHGEKEVELTLIPDSVEADL-ANTTCHVENNGR- 339
Qy 342 AKAAVKOKVAPARYVELACGFGATVLLVILIVVHVWLMVLFYRAHFGTDETLID 401
Db 340 -KHAIVLARKKOLIKIELAGLGALFLLIILLVYKCYNIEMLPYKORFGDDETTD 398
Qy 402 GKEDYIYVSAR-----NAEEBFVLLTRGVLENEFGYKLCIPDRSLPGNTVE 452
Db 399 NKEVAYLSYTKVQDDTLDCDNTVEEQFALIELPDLVLEHGYKLPFIPRDLIPSGTYIE 458
Qy 453 AVFDIORSRMIVLSPDYTEKISMLPEFKLGWCONSIAT--KLIVERYRLEPHH 509
Db 459 DLTRCEOSRRLIVLTPDYILRRGWSI--FELSRILNMLVSGEIKVILIBCTELK--- 513
Qy 510 PG-----ILQKESV--SFVSMGKESKHSKFKMALARLPLRSLASAGNMSGS 560
Db 514 -GKVNCOVESLKHNIKLISLIMKOPKSKLNSKFMALVYEMPIKKEMLSHCIVLDS 572
Qy 561 SOSDISLDHVORRSRLKEPPELOSSERRAAGSPAPAGMSKIRGKSATCRCCVYCEG 620
Db 573 AEOGIF-----GELQIPSIAMTSTSATVPSQADLPETHHSDSMQMRIC---CRGY 621
Qy 621 NH 622
Db 622 QH 623

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RESULT 9

Q9NZNI PRELIMINARY; PRT; 696 AA.

Q9NZNI;
01-OCT-2000 (Tremblrel. 15, Created)
01-OCT-2000 (Tremblrel. 15, Last sequence update)
01-JUN-2002 (Tremblrel. 21, Last annotation update)
X-linked interleukin-1 receptor accessory protein-like 1.
IL1RAPL1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_Taxid=9606;
[1]
SEQUENCE FROM N.A.
RP MEDLINE=20218565; PubMed=10757639;
RA Jtn H., Vismesvarajah R., Gardner R.J., Roberts R.G.;
RT "Two novel members of the interleukin-1 receptor gene family, one
deleted in Xp21.3-Xp21.3 mental retardation."
RL Eur. J. Hum. Genet. 8:87-94 (2000).
DR EMBL, AF181284; AAF59411.1;
DR InterPro; IPR003598; 19.C2.
DR InterPro; IPR003006; 19.MHC.
DR InterPro; IPR004075; IL1 receptor.
DR InterPro; IPR000770; SAND_domain.
DR

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DR InterPro; IPR000157; TIR_domain.
DR Pfam; PF00047; Ig_2.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PR01537; INTRLNRIIP.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00258; SAND; 1.
DR SMART; SM00255; TIR; 1.
DR Immunoglobulin domain; Receptor.
SQ SEQUENCE 696 AA; 79979 MW; F2EBCC37153799A0 CRC64;

Query Match 21.0%; Score 769.5; DB 4; Length 696;
Best Local Similarity 29.0%; Pred. No. 1.5e-56;
Matches 206; Conservative 127; Mismatches 287; Indels 91; Gaps 21;

Qy 1 MTLNVCVSLYFYGIQSDASERCDWGLDTRQIQVEDEPARIKCPLFEHFLKFNST 60
Db 8 LILLVATFQSLKXYTKGSDAGCTDMSID-IKKYQVAVGEVRIKCLFYGYIRNTSL 66
Qy 61 AHSAGLTIWTRDRLDLEEPINRLPENRISKEDVLMFRPTLLDNTGNTCLMRT 120
Db 67 AQSAGLSLMTYKSSGPGDFEPIAF--DGSIRMSKEBSIWFAPRTLLQDSGLVACVIRNST 124
Qy 121 YCSKVAAPLEVVOKDS--CFNSPMLPVHKYIEYG---LQICPNVDGFPSVYKPT 174
Db 125 YMKVVISLTVGENDTGLCTNSKMK-----YFEKAEISKEISCRDIBDPLTPREPE 178
Qy 175 ITWMCYKIQNFNNVIEGNNLSFLIALISNNGNYTCVVYTPENGRTFHLTRTLTKV 234
Db 179 ILWYECRTKTRPSIVKRPDITLLREVREDIGNYTELAK--CGFVVRRTTELTLTV-- 234
Qy 235 GSPKQANP-PVHSNDHNVYKEKEGELLIPCTVYPSFLMSDNEVWMTIDGKPPDI 292
Db 235 -APLTDKPKPLYPWESKLTIOETQDGSANLTCRAFGYSGDVAPLLIYMKGEKFEIDL 293
Qy 293 ----TIDVTINESISHRTEDTRTQIISIKKVTSEDLKRSYVCHARSAGVAKAK 346
Db 294 DENRVESDRI--LKEHLGEQVYSISLI--VDSVEBDL-GNVSQVYENGNGR--RHAS 346
Qy 347 VKOKVAPARYVELACGFGATVLLVILIVVHVWLMVLFYRAHFGTDETLIDGKED 406
Db 347 VLMHRELMYVELAGLGALILLVCLVYIKCKYKIMLFYRNHFAEELDGNKOYD 406
Qy 407 IYVSAR-----NAEEBFVLLTRGVLENEFGYKLCIPDRSLPGNTVAVPDF 457
Db 407 AYLSTKYDPPQWQNETGEERFALIELPDLVLEHGYKLPFIPRDLIPGTYIEDVARC 466
Qy 458 IQRSRMTIVLSPDYTEKISMLPEFKLGWCONSIAT--KLIVERYRLEPHHGLQ 514
Db 467 VDQSRLLITVMTPNVVRGWSI--FELSTRRLNMLVTGEIKVILIECSELR---GIMN 520
Qy 515 LKE-----SVSFVSMGKESKHSKFKMALARLPLR----- 547
Db 521 YQVEVALKHTIKLIVIMHPKCNKLNKSKFMALVYEMPIKKEMLSHCIVLDS 580
Qy 548 --SISASGMSGSSGSDISLDHYQR-----RSFLKEPPELOSSERRAAGSPAPAGX 598
Db 581 FGEIQTVAISMAAATSTALTAHPDLRSTYNTYHSGMRQKHYRSEYEVV--PRTGTL 638
Qy 599 MSKIRGKSATCRCCVYTPENGRTFHLTRTLTKV 649
Db 639 PLTSGINQHTYCNIPMTLINDQRPQYSSRQNDPEAHNTASAILPLPRET 689

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RESULT 10

Q9U53 PRELIMINARY; PRT; 696 AA.

Q9U53;
01-MAY-2000 (Tremblrel. 13, Created)
01-MAY-2000 (Tremblrel. 13, Last sequence update)
01-JUN-2002 (Tremblrel. 21, Last annotation update)
OLIGOPHRENIN-4 (TIGIR-2).
GN OPN4.
OS Homo sapiens (Human).
OS


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QY 294 IDVTINESISHSRTDETRT-----QILSIKVTSEDLKRSYVCHARSAKGEVAKAA 345
DB 261 I-----HEEKEMKIMTPEGMKASKVLRLENIGESMLNLYNCTVASTGTDTKSF 311
QY 346 KVKOK-----VPARYVELACGFATVLL-----VVLIVVHYVWLEMLVLYRAHFGTDE 397
DB 312 ILVRKAMADIPGHVFT-----RGMIIVALLIVAVCVIYRVDLVLYFRLTLRDE 367
QY 398 TIIDKEKDYIVYAR-----NABEEFVLLTGLVLENEFGYLCIFDDSLFGAGTVR 452
DB 368 TILDGKYDFAVSYLKCRCPENGHEHTFAVEIILPRVLEKHGTYDLCIFERDVVPGAVVD 427
QY 453 AVDFIORSRMIVLSPDVVTEKSIEMLEPK-GVMCONSIAFKLIVREYRPLEHHP-- 509
DB 428 EHSLEKSRRLIIVLSKSTNSNEVRYELBSGLHEALVERKI--KITLIEFTPTDFTL 485
QY 510 PGILQLKESVSPVSWKESKSGSKFWMKALRLALPLRSL 549
DB 486 POSLKILKSHRVLKWKADKSLSYNSRFMKOLLVLMPAKTV 525

RESULT 12
3874
Q09874 PRELIMINARY; PRT; 555 AA.
AC 090874;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE IL-1 receptor I precursor.
GN IL-1 RECEPTOR I.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92175529; PubMed=1531799;
RA Guida S., Heguy A., Meili M.;
RT "The chicken IL-1 receptor: differential evolution of the cytoplasmic
and extracellular domains.";
RL Gene 111:239-243(1992).
DR EMBL: M81846; AAA8924.1; -.
DR HSSP: P14778; 1ITB.
DR InterPro: IPR003599; IG.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR004075; IL1_receptorI.
DR InterPro: IPR004074; IL1_receptorI/1.
DR InterPro: IPR000157; TIR_domain.
DR Pfam: PF00047; Ig_2.
DR Pfam: PF01582; TIR_1.
DR PRINTS: PRO1536; INTRLNRI12P.
DR SMART: SM00409; IG_1.
DR SMART: SM00255; TIR_1.
DR Receptor: Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 555 IL-1 RECEPTOR I.
SQ SEQUENCE 555 AA; 63995 MW; 4DB56DD7B1BB17AA CRC64;

Query Match 13.5%; Score 496; DB 13; Length 555;
Best local Similarity 26.4%; Pred. No. 1.9e-33;
Matches 155; Conservative 109; Mismatches 230; Indels 94; Gaps 26;

DB 26 CVICNYP-----VLGEPYALSCP-----ITLPMHS-D 54

QY 6 CVSLYFYGILQSDASERCDDMDLDTMRQIQVFEDEBARIKCPLEHPLKFNSTASHAG 65
DB 26 CVICNYP-----VLGEPYALSCP-----ITLPMHS-D 54

QY 66 LTLIVYTRDRLDEIRINRLPENRISKEDVUWFRPLTNDGNTQALRNTTYTSKY 125
DB 55 YNLITWY--RNGSNM--PITTE-RRARIHQKGLMFLPALLESGLICEVRSIRNSKOK 109

QY 126 AFPLEVVOKDS--CFNSPMKLPVHKLYIEVGIRITCPNDGY-FPSAVKPTITWYNGCY 182

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DB 110 IINLKVFNKNDNGLCFNGEKK--YDQIVSANAGKIIICPDLNFKDNDINPEIHHYKECK 167
QY 183 K--IQNFNNVITPEGMN-LSFLIALISNNNGTCVVTYPENGTFLTRLYKVVSGSPK 239
DB 168 SGFLEDKRVLVLEGEBAIILINVTIIOCKNTYCRWVYTYTMGQYVNSRTPMLEVKSPLK 227
QY 240 AVPVTHSPNDVHYVEKEGEELIPCTV---YFSFLNDSRBNWMTIDGKKPDDITIV 296
DB 228 MREFTY-PNNNTI-EVELGSHVMECNVSSGYGL-----PYMQVDEVD--SFDS 277
QY 297 T-----INESISHSRTDETRTQILSIKVTSEDLKRSYVCHARSAKGEVAKAVKQKV 351
DB 278 TYREQPEEGMHPGIAVSGTK---FNISVKKQDYAVKFCFIYDSQFTSYIQLHE-- 332
QY 352 PABRYVELACGFATVLLVVLIVVHYVWLEMLVLYRA--HFGTDETIIDKEKDYIV 409
DB 333 PVQNINGVYLIGGDISLIFLPLIIVYKIFKIDIVLMYRSSGHPILGKKVSGDKIYDAVY 392
QY 410 SYARNR-----EEFVLLTGLVLENEFGYLCIFDDSLFGAGTVR 464
DB 393 LYPKNRSECLYSSDIFALKILPEVLERQCYNLFIYGRNDLGEAVIDVDEKIHQSRKV 452
QY 465 IIVLSP-----DYTEKSIEMLEPKLGVWCCONSIAFKLIVREYRPLE--HHPGIL 513
DB 453 IITLVEPCTGILBESKHLAV-----YNALIDGI--KITLIEKIEDVANNPESIK 506
QY 514 QLKESVSPVSWK--EKSNGSKFWMKALRLALPLRSIASSGWNES 558
DB 507 YVQKYGALRMTCDFPERSHASTRFMKVRYHMSRKRKSSSGPILS 554

RESULT 13
Q61098 PRELIMINARY; PRT; 537 AA.
AC 061098;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE IL-1RTP precursor.
GN IL18R1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96223957; PubMed=8626725;
RA Parnet P., Garka K.E., Bonnet T.P., Dower S.K., Sims J.E.;
RT "IL-1RTP is a novel receptor-like molecule similar to the type I
interleukin-1 receptor and its homologues TI/ST2 and IL-1R AcP.";
RL J. Biol. Chem. 271:3967-3970(1996).
DR EMBL: U43673; AAC52437.1; -.
DR HSSP: O60603; 1FYW.
DR MGD: MGI:105183; 118R1.
DR InterPro: IPR003600; IG_1like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR004075; IL1_receptorI.
DR InterPro: IPR000157; TIR_domain.
DR Pfam: PF00047; Ig_3.
DR Pfam: PF01582; TIR_1.
DR PRINTS: PRO1537; INTRLNRI1P.
DR SMART: SM00410; IG_1like; 1.
DR SMART: SM00255; TIR_1.
DR Signal.
FT SIGNAL 1 18 POTENTIAL.
SQ SEQUENCE 537 AA; 61600 MW; B119FEA40335458 CRC64;

Query Match 13.1%; Score 479; DB 11; Length 537;
Best local Similarity 27.4%; Pred. No. 5.1e-32;
Matches 167; Conservative 102; Mismatches 218; Indels 122; Gaps 30;

QY 1 MTLIMCVSLYFYGILQSDASERCDDMDLDTMRQIQVFEDEBARIK-----CPLFEHPLK 55

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Db 6 LILTLCL:-----LIVSASKSCIH-----RSQIHVVEGEFPYKPCGISAPVARN--- 50
Qy 56 FNVSTASHAGLTLVWTRORDLEEPINFLPENRISKEKOVLMFRITLNDTCNYCM 115
Db 51 ---ETA-----TMRWFKSGASHRELNRRSP--RVTFHDHTLEFWPEWEDGETYISQ 100
Qy 116 LRNTTYSKVAFLPEVVO--KDSCFNSPMKLPHKLYIEYGIO-----RITC--PNVGY 166
Db 101 VGN-----DRRWTLNVTNRKNSHSCSD-----KLVTSDPEVVKSLHITCKNPVTEEL 149
Qy 167 PPSVSKPTITW-YMGCYKIQNFNNVIEPGMNLSPILALISNNNGTCCVVTYPENGRTFL 225
Db 150 IOD-----TWLYKNCKEISKTPRILKD-----AERGDEGYSCVFSVHNQTRVNI 195
Qy 226 TRITLVKVGSPKNAVPPVISHPNHVYKEKPEGBELIPCTVYVSFLMDSNENWMTID 285
Db 196 TKTVNITVYI-EGRSKVTPALIGPKCEKV-GVELGQDVELNC-----SASLMDODLFPYMSI- 248
Qy 286 GKXPDITIDVTINESISHSRTDET-----RTQILSIKVTSEDLKSYVCHARSA 337
Db 249 -RKED-----SSDPNVEDRKETTWTWSEGLHASKILRFQKITEVNTLVNCTVANE 301
Qy 338 KGEVAKAKVQK---VPAPRYVELACGFGATVLT-----VLLIVVHYVWLEM 385
Db 302 EADTKSFVLVRKEIPDIRGHVFT-----GGVTVLVASVAACVILCVIYKV---DL 352
Qy 386 VLFPAHFGTDETLIDKEVDIYVSAR---NABEEFVLLTLRGVLENEFGYKLCIF 440
Db 353 VLFPRILAEDETLIDGKYTAFVSYLKECPENKEEYFAETTLPRVLEKQFGYKLCIF 412
Qy 441 DRDLPGNTVEAVDFIORSRMTVLSPOVTEKISIMLEFLK-GVMCONSITKILIV 499
Db 413 ERDVPPGAVVEHSHLSKSRRLITVLSQSTLTNGARRELSGHEALVEKXI--KILL 470
Qy 500 VEYRPLEHPH--PGIILQKESVSEVSWKGEKSKHSGKFWKALRLALPLRSLSASSGANE 557
Db 471 IEFPPASITFLPSPILKILKSYRVLKWAD--SPSNKSRFWKLVYLMRAKAVKP---WRE 526
Qy 558 SCSSODIS 566
Db 527 ESEARSVLS 535

**RESULT 14
1208
AC Q05208 PRELIMINARY; PRT; 567 AA.
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE ST2L protein precursor.
GN ILRL1 OR ST2L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93170492; PubMed=7916701;
RA Yanagisawa K., Takagi T., Tsukamoto T., Tetsuka T., Tomimaga S.;
RT "Presence of a novel primary response gene ST2L encoding a product
RT highly similar to the interleukin 1 receptor type 1."
RL FEMS Lett. 318:83-87(1993).
DR EMBL; D13695; BAA02854.1; -.
DR MGD; MGI:98427; ILRL1.
DR InterPro; IPR003598; IG_C2.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR004075; IL1_Receptor1.
DR InterPro; IPR002052; N6_Mease.
DR InterPro; IPR000157; TIR_domain.
DR Pfam; PF00047; Ig; 2.
DR Pfam; PF01582; TIR; 1.

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DR PRINTS; PR01537; INTRLNRLIF.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
KW Immunoglobulin domain; Signal.
FT SIGNAL 1 17
FT CHAIN 18 567
FT ST2L PROTEIN.
SQ SEQUENCE 567 AA; 64801 MW; 9228CE227D95B0BC CRC64;

Query Match 13.04; Score 478; DB 11; Length 567;
Best Local Similarity 25.94; Pred. No. 6,7e-32;
Matches 163; Conservative 105; Mismatches 227; Indels 134; Gaps 28;

Qy 4 LM--CVSLVYFGILOSASRCDDMGIDTMRQIQVEDEPARIKCPLEHFLKFNYSYA 61
Db 9 LMAALITLPMY-LITVEGSK--SSKGL-----ENELIYRCF-----QGRST- 49
Qy 62 HSAGLTIWTRORDRDLPEEPINFLPENRISKEKOVLMFRITLNDTCNYCMRLNTTY 121
Db 50 ---YPEWYVS-----DTNESIPTQ--KRNRIFGSRDLKFLPAVVEBGIVACYRSPNL 100
Qy 122 CSKVAFLPEVVOQDSRNSPMKLPVHKLIEYGIQR-----ITCPNVGIFPSSVYKPT 174
Db 101 NKTGYLWVTHHKKEPPSCNIPD-----YLMYSTVRSGDKNFKITCPTIDLY--NWTP 150
Qy 175 ITWVGCYKIQN-----FNNVIEPGMNLSPILALISNNNGTCCVVTYPENGRTF 223
Db 151 VQWFKNCALQEPFRRAHSTYLFIDNVTHD-----DRGDYTCQTHANGNTY 198
Qy 224 HLTRTLVKKVGSBKNAVPPVISHPNHVYKEKPEGBELIPCTVYVS---FLMDSNNE 279
Db 199 IVTATREFTVEKSPMFVITNPYNHTM-EVEIGKPAISACACROKSGHFLAD----- 253
Qy 280 VMTTIDGKPDITIDVTINESISHSRTDE-----TRQILSIKVTSEDLK 327
Db 254 VLM-----QINKTVGNFGEARIOEBEGNESSNDMDCLTSVLRITGVTEKXLS 303
Qy 328 RSYVCHARSAKGEVAKAKVQKVPAPRYTV-ELACGFGATVLTLLIVVHYVWLEMV 386
Db 304 LEYDCLALNLMGMTIRLTRLRKOPIDHRSIYIVAGCSLLMTNLTNVLVLAQFWLEVA 363
Qy 387 LFPYAHFGTDETLIDKEVDIYVSAR---NABEEFVLLTLRGVLENEFGYKLC 438
Db 364 LFMWDIYTPYKTRNDGKLYDAIYIYPRVFRGSACTHSEVFVHHTLPDVLNCGYKLC 423
Qy 439 IEDRSLPGNTVEAVDFIORSRMTVLSP-----DYTEKISIMLEFLKGVMCNS 492
Db 424 IYGRDLLPGQDAATVVESSIONSRQVFLVAPHMHSKEFAVEODIAL---HSLALQNN 479
Qy 493 IATLIVYERPL-EHHPGILQKESVSF-----VSWKGE--GSKHSG-KSPFWKALR 541
Db 480 --SKVILILEMPELGEASRLQVGDLSLQHLVKIQGTIKMREDHVADKQSLSSKFWKVR 537
Qy 542 LALPL-RSLASGNNSSCSQSDISLDH 569
Db 538 YQWVPERASKTASVAPLSKACLDLKH 566

**RESULT 15
09TV71
AC Q9TV71 PRELIMINARY; PRT; 573 AA.
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE Interleukin-1 receptor type I precursor.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxId=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Kirisawa R., Hashimoto N., Sakamoto C., Enya S., Hagiwara K., Iwai H.;

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RT "Molecular characterization of the equine type I interleukin-1
receptor cDNA."
RL Submitted (NOV-1998) to the EMBL/Genbank/DBD databases.
DR EMBL; AB020338; BAA83730.1; -.

DR HSP; P14778; IIRa.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR004076; IL1R_receptor.
DR InterPro; IPR004075; IL1_receptor.
DR InterPro; IPR004074; IL1_receptor1.
DR InterPro; IPR000157; TIR_domain.
DR Pfam; PF00047; TIR; 1.
DR PRINTS; PR01538; INTERLEUKIN1.
DR PRINTS; PR01536; INTERLEUKIN1F.
DR PRINTS; PR01537; INTERLEUKIN1P.
DR SMART; SM00410; IG_like; 2.
DR SMART; SM00255; TIR; 1.
DR Receptor; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 1 573 MATURE INTERLEUKIN-1 RECEPTOR TYPE I.
SQ SEQUENCE 573 AA; 65766 MW; 25703365A89B230B CRC64;

Query Match

13.0%; Score 477.5; DB 6; Length 573;

Best Local Similarity 25.8%; Pred. No. 7.5e-32;
Matches 153; Conservative 120; Mismatches 224; Indels 97; Gaps 27;

QY 4 LMCVSVLYYYGILQSDASRCDDWGLDMRQIQVFEDEPARIKPLFEHFLKNYSTAHS 63
DB 7 LVCFLIAL----LISLEADKCEERGEPIVIVSAYRIDVR--SCPL-----NPNB 50
QY 64 AGLTLIYWTRODRDLKEPINFRLPENRISKEQVLMFRPTLLDNGANTYQMLRNTYCS 123
DB 51 SNGTIIWY----KNDSETPVSMK--KDSRIHQYDKLWFPVPAKIBDSGHYCAVRNSTYCL 105
QY 124 KYAFPLEVVO--KDSCEFS----PMKLPMHKLIEYGIORITCPNVGYPSSVK--PTIT 176
DB 106 KYKITARFQHEPDLQYNAQALFTQCLPIG----EDGL--LVCPIYLFVRDENNELPKIQ 159
QY 177 WTMGCK--IQPNNVITPFGANLSFLIALI--SNNGNYTCVVTYPENGRTFHLFRTLTVK 232
DB 160 WYKDCOPLIDNINFI--GKTDKLIWANVTEAHKGYTCHISYTHGKQYPTITVIGLI 216
QY 233 VVGSPKNAPVPIHSPNDHVVYEKEGEELLPCPTYPSFLMDSRNEMWTTIDGKKPDI 292
DB 217 TIDEIRPTPLIVSPVNE--TMEVDLGSOVOLICNVYGMF---TDVYWRNNGSLIDD- 269
QY 293 TIDVTINESI---SHSRTEDETRTOILSIKYVSEDLKRSYVCHARSAKGEVAKAKVK 348
DB 270 -SDPVLVEYKKEVENSLKRRHTLITVLANISAVESRFYIYPTCLAKNSYGRSAAYQUR 328
QY 349 QKVPAARYVELACGEGATVLLVIL--IVYHYVLEMLFYR--AHFGTDETLIDGK 403
DB 339 QEVPDFQKHV-----IGIFVLLVLAITCSVFYIKLFKVDLVLMYRDSCYDFRSPKASDK 383
QY 404 EXDIYVSVAR-----NAEEEFULLTLGVLENERGYKLCIPDRDSLPGNTVEAVPDF 457
DB 364 TYDAIYLYKIIIGEGSTNSDIFVFQVLPVELEKQGGYKLFYGRDYYGEDIIVEVTNEN 443
QY 458 IORSRRMIVVLSPD-----YTEKSIEMLEFKLGVMCONSIAWKILIVEYRPLEHPH 509
DB 444 IKSRRLIITIVRETSGLSWLSSSSEQIAM-----YNLVQDGI--KIILLELEKIODEY 497
QY 510 PGILQAKESVSFVS-----WKGEKSK--HSGKFWKALRLALPLKSLSSAS 553
DB 498 ---KMPESIKRPIKRGHGLRWSGDSRKGPOSAKARFWKRVYRMPVQROLPS 547